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(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1- 468 or the complement thereof. The invention relates also to polynucleotides arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
15 survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

20 Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
25 new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
30 into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex)
20 wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10 libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences of the invention wherein the amount of reaction product of

15 step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particular useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ; SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
10 SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14 ;
SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

The invention relates also to a method of detecting
25 differentially expressed genes correlated with a cancer
comprising detecting at least one library of polynucleotide
sequences as above defined or of products encoded by said
library in a sample obtained from a patient.

A particular embodiment of the invention relates
30 to a polynucleotide library of corresponding substantially to
any combination of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets 1 to set 212 as defined in
table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence
5 selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of
10 genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
15 table 6
20

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.
25
30

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from antracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

30 The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF β 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

15

20

25

30

the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFB3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

 Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating rate, favorable prognosis and response to hormonal therapy. 10 The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes 15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other 20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in 25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high 30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XPB1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cl1/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, subfamily b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBPI	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (LI-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (IT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:418
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246820	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pl (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDP2	19	actonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Ttk2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112822		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFB3	42	transforming growth factor, beta receptor III (TGFB3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192888		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	Epha2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	CAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	138326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	305943	SEQ ID No : 89		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbol gene	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141824		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	190282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1)(ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	y-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	183380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:168
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:406
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating)	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	Interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protelhe kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST AW184517	rien		Image ?					

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

5 SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ
ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74;
SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID
No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET
34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID
No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID
No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID
No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID
No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET
10 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:78) ; SET 42: (SEQ ID
No:102; SEQ ID No:103) ; SET 43: (SEQ ID No:104; SEQ ID No:105) ;
SET 44: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 45:
(SEQ ID No:109; SEQ ID No:110) ; SET 46: (SEQ ID No:111; SEQ ID
No:112; SEQ ID No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID
15 No:115; SEQ ID No:116; SEQ ID No:117) ; SET 49: (SEQ ID No:118;
SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51:
(SEQ ID No:122; SEQ ID No:78) ; SET 52: (SEQ ID No:123; SEQ ID
No:124; SEQ ID No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127;
SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55:
20 (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID
No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ;
SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59:
(SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID
No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147;
25 SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID
No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154;
SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID
No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ;
SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164;
30 SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID
No:152) ; SET 69: (SEQ ID No:168; SEQ ID No:169; SEQ ID No:170) ;
SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173;
SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID
No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID
35 No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183;
SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186)
; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:263; SEQ ID No:264) ; SET 111: (SEQ ID No:265; SEQ ID No:266) ; SET 112: (SEQ ID No:267; SEQ ID No:268) ; SET 113: (SEQ ID No:269; SEQ ID No:270) ; SET 114: (SEQ ID No:271; SEQ ID No:272) ; SET 115: (SEQ ID No:273; SEQ ID No:274) ; SET 116: (SEQ ID No:275; SEQ ID No:276) ; SET 117: (SEQ ID No:277; SEQ ID No:278) ; SET 118: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 119: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:284) ; SET 120: (SEQ ID No:285; SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 121: (SEQ ID No:289; SEQ ID No:290) ; SET 122: (SEQ ID No:291; SEQ ID No:292) ; SET 123: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 124: (SEQ ID No:296; SEQ ID No:297) ; SET 125: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 126: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 127: (SEQ ID No:303; SEQ ID No:304) ; SET 128: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:
5 (SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID
No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450) ; SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

20 7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim
5 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10 12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each
15 one of predefined polynucleotide sequences sets comprising:

20 SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET
25 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),
30

wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
10 No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106;
SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID
No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ;
SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No
5 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ
ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96
(SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID
No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258)
; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID
10 No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276)
; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID
No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296;
SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID
No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344)
15 ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID
No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363;
SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID
No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108)
; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET
20 No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166
(SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID
No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401)
; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET
No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173
25 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID
No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424;
SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID
No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184
(SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

30 wherein said sequences are useful in classifying
good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim
20 wherein said polynucleotide sequences or subsequences
35 thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

5

Figure 1

Figure 1A Normal Breast

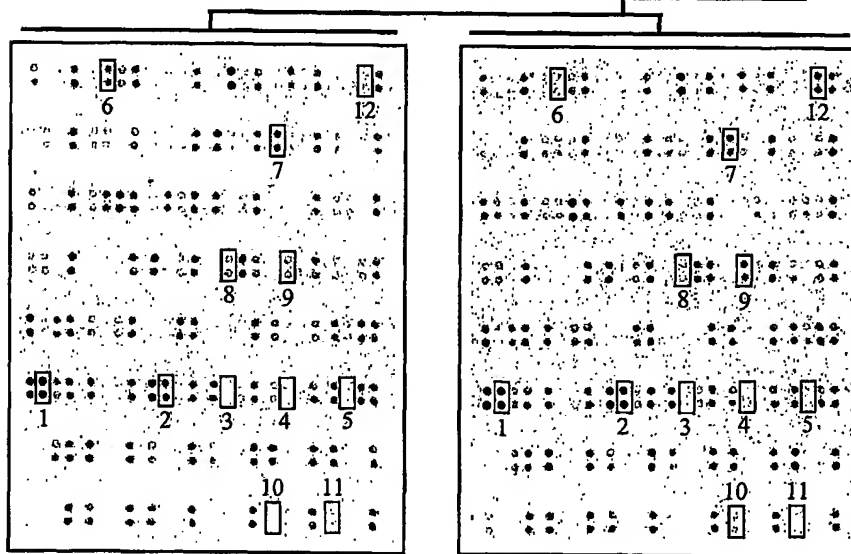
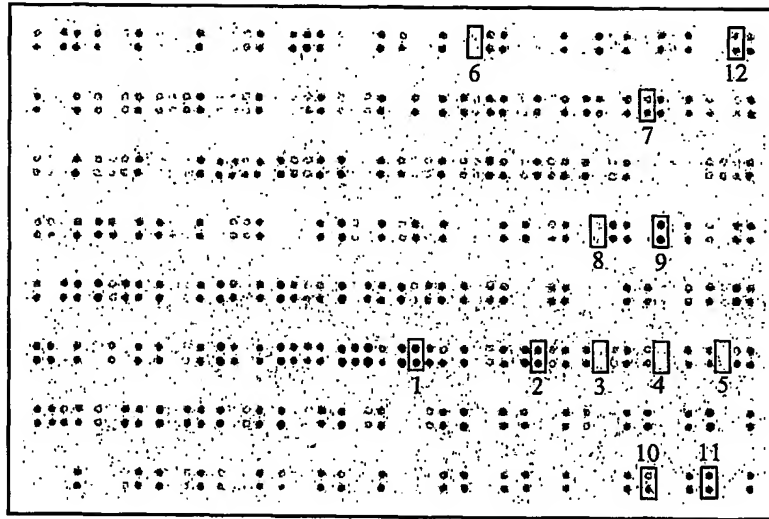


Figure 1B ER-

ER+ Figure 1C

Breast cancer

Figure 2

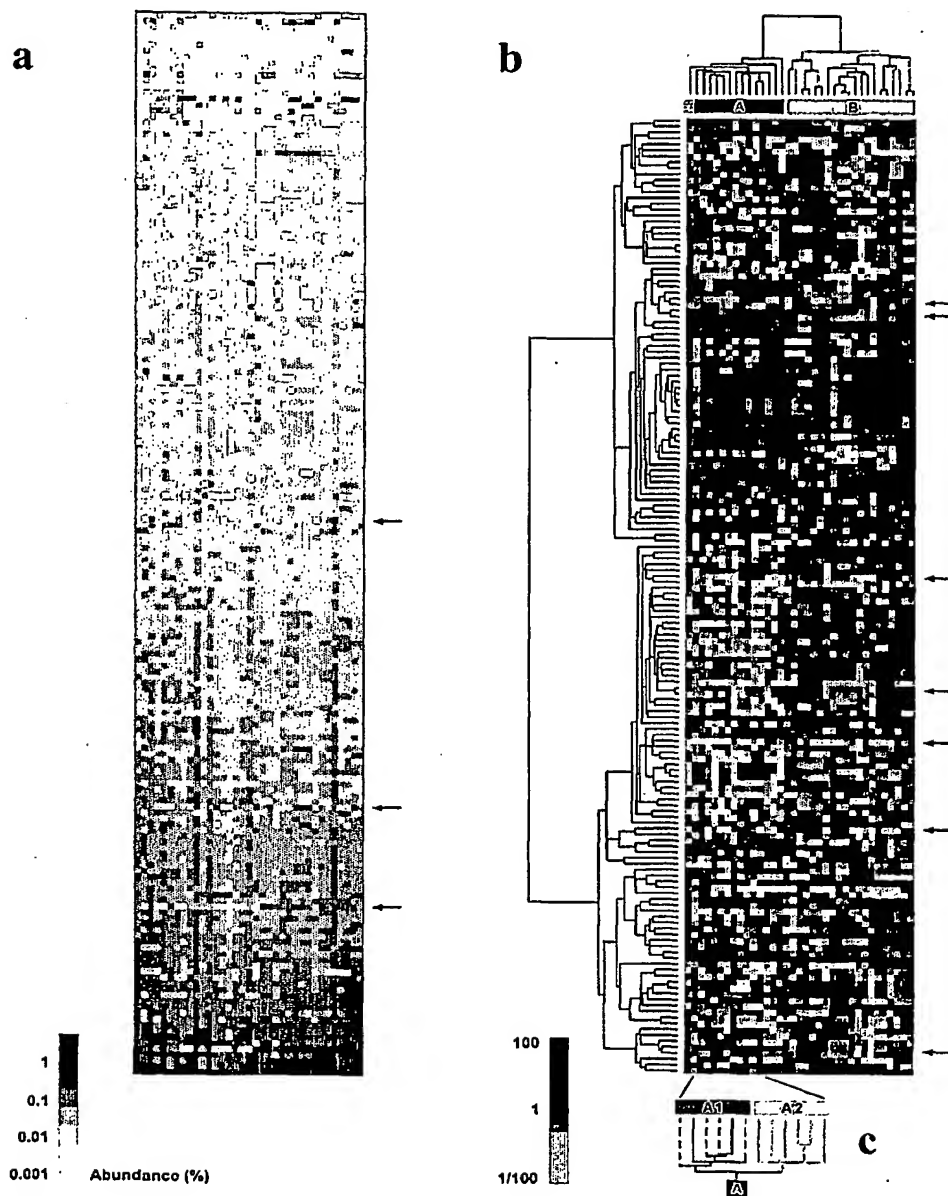


Figure 3

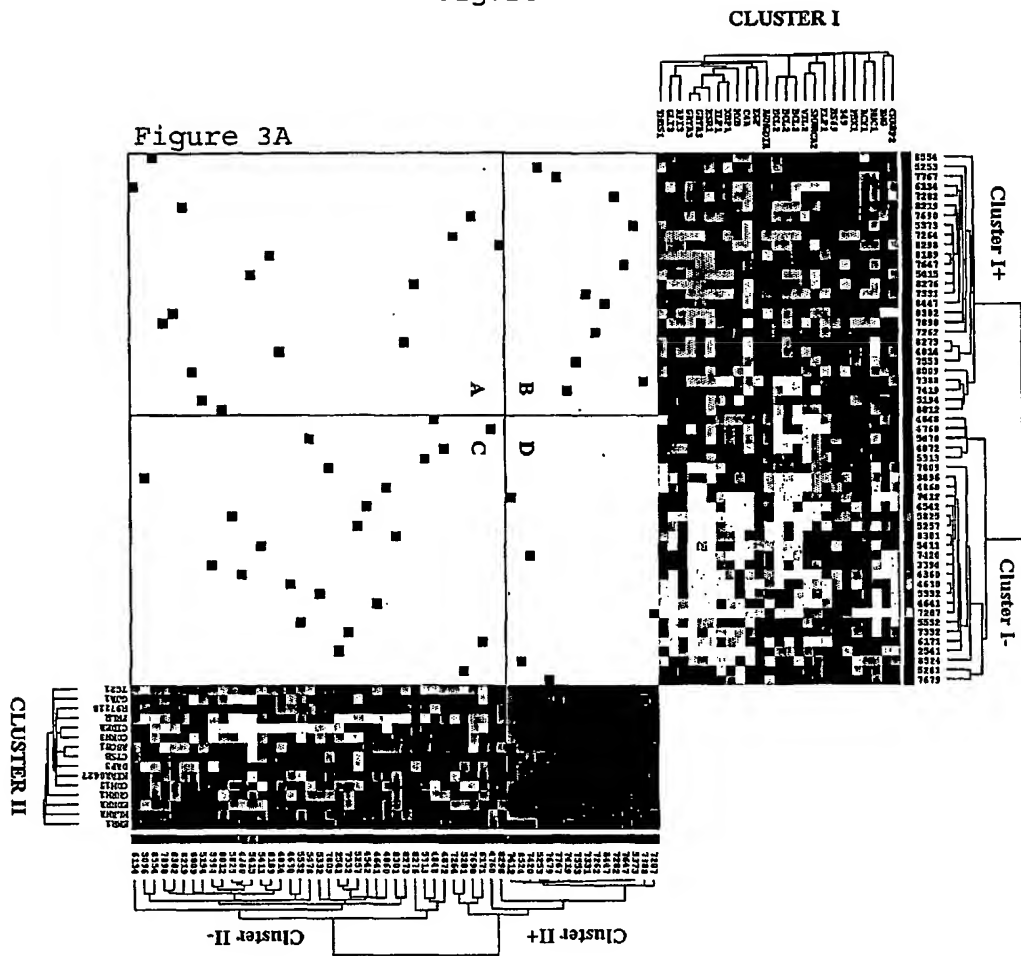


Figure 3C

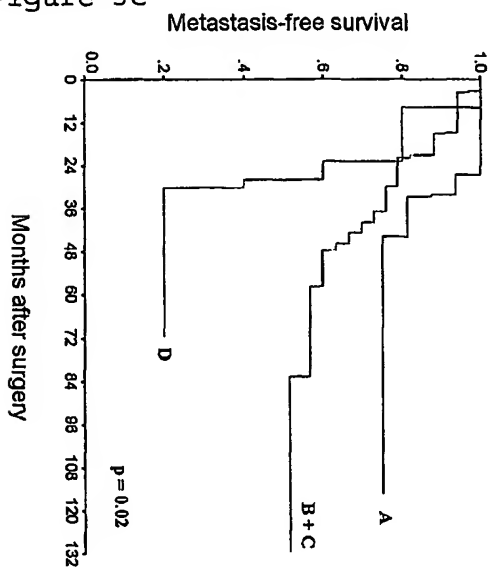


Figure 3B

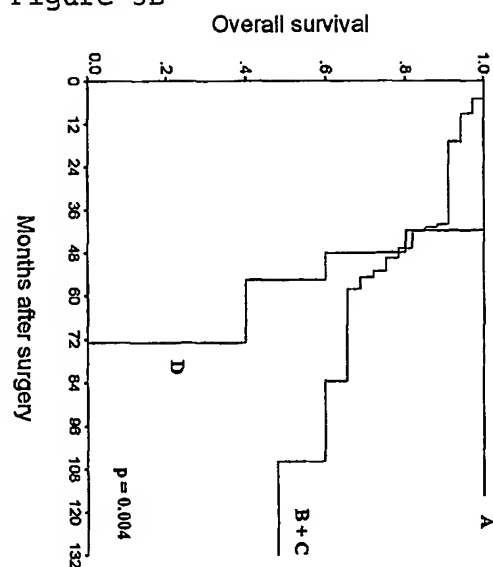


Figure 4

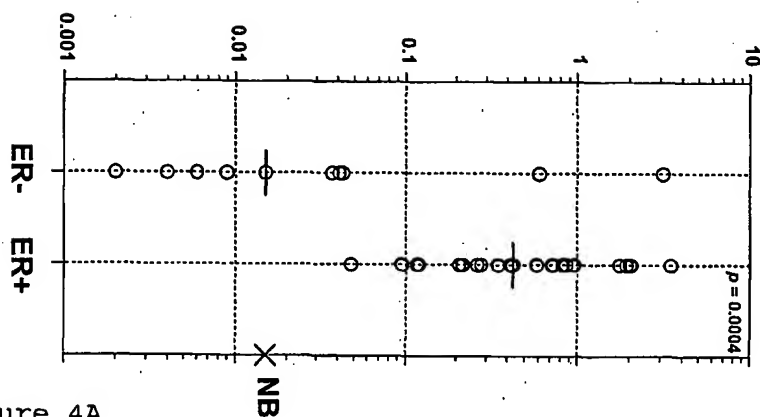


Figure 4A

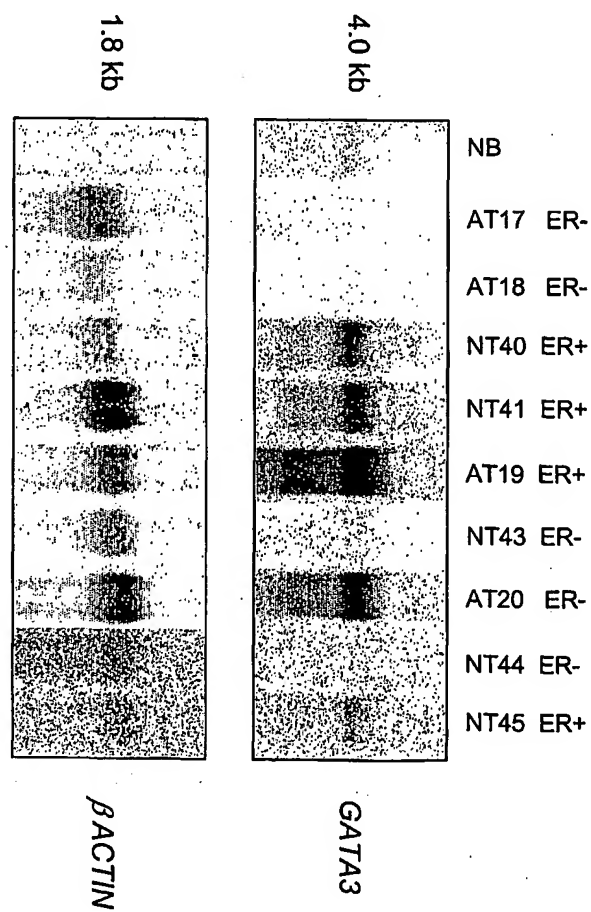


Figure 4B

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<110> François Bertucci
Rémi Houlgatte
Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

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<130> 10813PCT-December-2001-ipsogen

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2/292

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ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtggg caaatggcgt tcagcagcgg 2460
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aaaggttcat ctgtccatgc aaaaaaa 3327

```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac aggggttnngc acattgccca ggatggtctc aaactcctag agttgagcta 60
tccacccacc tttggcctnc caaagtgtct ggatcacagg cgtgagtcac tgnntccagc 120
acccatctgg aggtcttctta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggcccc 240
ctttgaagaa ccactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8

```
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tctctttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt                                     369
```

<210> 9

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(255)

<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9

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aaagacagtt tttgggtaat cttttncttt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc cctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc                                     255
```

<210> 10

<211> 1325

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1325)

<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

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gcgcgggggca gcagaagcga gagccgagcg cggacccagc caggaccac agccctccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgca agtgaaacc 180
atccgccgag cgtacccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcggaag agacctgcgc gccctcggtg tcctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcct gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctctggtga acaagctcaa gtggaacctg 600
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gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
gtggcctcatg tttccaatcc gccctccatg tgggcagcgg ggagcgtggt ggccgcagt 780
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cggccccagg tgctccacat gacagtcctt cctctccgga gcattt tgat accagaaggg 1140
aaagcttcat tttccttgtt ttggttgggt ttttctttg ctctttcccc cttccatctc 1200
tgacttaagc aaaaagaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325
```

<210> 11
<211> 449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(449)
<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

```
<400> 11
atttgaagt caaagtotta tttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagctt ggcggctgaa tttcggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggttaatt gacctcgaga cgacctctct gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccag cggttggggc ctccattcct ttgggtacaa 360
catgctgggt ngcggggaac ccgggg antc tgttccttnt ttcctggact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt 449
```

<210> 12
<211> 4003
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

```
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gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctogacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cccttgttgg 180
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ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgttta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttggagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaaat 540
tctgaaaaac gccagagatg ttaat caggc tcagtcgggg aatattcaga gcacagtgat 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
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aaccttgca gacagagaac acgagaccaa tgggtgtggc aagagtgatc agaaacaaga 780
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gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attaggtgtg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
```

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```

ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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```

<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,
keratinocyte growth factor receptor, craniofacial
dysostosis 1, crouzon syndrome, pfeiffer syndrome,
jackson-weiss syndrome) (FGFR2) gene.

<400> 13

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attaaaaaaa gagagaccaa tttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttatttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,
keratinocyte growth factor receptor, craniofacial
dysostosis 1, crouzon syndrome, pfeiffer syndrome,
jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggac 60
tggtggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttgatc 120
gaattctcac tctcacaacc aatgaggaat acttggaact cagccaacct ctggaacagt 180
attcacctag ttaccttgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaaccatgcc ttcctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgncccaa acaggacag gcactggggg 360
aacctaggct acattnagga aggggaggac cttgccttc ccaggngttt gttt 414

```

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<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 15
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gcgtacctgg cccggcgcgg cgactgctct c cgggctggc gggggccggc cgcgagcccc 120
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cccaccgcag gctgaaggca ttgcgcgtag tccatgccc tagaggaagt g tgcagatgg 540
gattaacgct cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
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```

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aaagagaata tttacaatat atgactaatt tggggaaaat gaagttttga tttatttgtg 3960
tttaaatgct gctgtcagac gattgttctt agacctctc a aatgccccat attaaaagaa 4020
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cccactcact ttgcaatagc cgtgcaagat gaatgcagat tacactgatc ttatgtgtta 4560
caaaaattga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
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<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctctcactt aatgctatta aaaaaaaatc tgatttggtg aattaacccc acttctcata 180
gtttaattgg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg gggctctgag gctgctgggg gtgatccga ggaacaagaa gctgccctat 300
taaaagttaat ctacttgagt tttcccgag tctttgggag ttgttcccta ctgtggggct 360
acttataggg gtagggcccc ccaaatccct cacacttagg tcggccctgc tggcttgctg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacct attttctggc 480

```

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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt ttacagaat 60
aaatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttggtt ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc cttgggtcgt cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggccac cagcgtgtat gc tacccttt cgggggtggg 300
cattcgctca ttaattcggg ccagncct cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttgagcac tatacccaca aactgtccg aggggtgtct tatttctaca gttaccctgc 60
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gcccacaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcatgaata tcaggcagtt taactgttct ccacaccctt actgggcttc 300
caaactttat gggatgtttt cacatgggtc ttgcctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tgntcaaca ttatggntct ggatggacgg aactgatttt 420
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnttaggttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```
ggccaccct tagcagcggc cgcggtcggc gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cgggtgggcc tcgtcctgtc agtggcgtcg gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcggc caccgctgag gagccggggc cgggcacggc 180
tggtgacggc ctccgggcag ctaaggctgc ccgaggagaa ggccggcggc gcggcgtagg 240
cgcacgtccg cggggctcct ggagcctgga ggaggccgag gggaccatgt ccgggaggcg 300
cttccacctc tccaccaccg accgcgtcat caa agctgtc ccctttcctc caacccaacg 360
gcttactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagtg 660
tgtgctgtat ttatggagtt taaagattaa tcatcccaaa acattgtttc tgcttcgggg 720
aaatcatgaa tgcaggcatc ttacagacta ttccaccttc aaacaggaat gtc gaatcaa 780
atattcggaa caggtgtatg atgcctgtat ggagacattt gactgtcttc ctcttgctgc 840
cctcttaaac cagcagtttc tctgtgtaca tggaggaatg tcacctgaaa ttacttcttt 900
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gcagaacaat aatttactat caattatcag agcccatgaa gcccaagatg ctgggtatcg 1140
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tttcacatgg tctttgcctt ttgttgggga aaaagtcaca gagatgctgg taaatgtgct 1380
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aattcttcgg caagaaagtg agagtgtgct gactctcaag ggcctgactc ccacaggcac 1560
actccctctg ggcgtcctct caggaggcaa gcagactatc gagacagcca tcagagggtt 1620
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gcgaatgcc accccgaaagg atagcatata ccctgggtgg ccaatgaaat ctgtaacctc 1740
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agtccctcgg tgctcaggtg gatctaaaac tcaagaacaa attctattta ttattatt g 1860
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aaaaagtga tctgttttgt tttcccttt tttctcata attttaagaa atgaatctga 2040
ttgttgtaaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttgga aa cctcaaacct gggtttctga cccc 2134
```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

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<400> 20

atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttggtg caatgggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttgngaataa atttntccaa 240
aaaaacca 248

<210> 21

<211> 427

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(427)

<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21

taagatacga acgagaaacc tgatttattg ctcaccttc ccttgccctcc ctaatggcaa 60
gcaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggta tattttaag 180
tagaataaca catgctgagt gtaaaactggg ctttgattg gtcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300
aaactggcta tgggtagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420
cctttga 427

<210> 22

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(294)

<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22

tttcttggtt ttcttttttt ttttccgaaa ccaactgccc tccactgact gccctgtac 60
cacatcaaac agtctcctct cctccaogcc tccggggtct gggaagtctc acctactga 120
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gtttgaccgt gaacccctt ccagttcgtg tcctcctccg cccccgcccc 240
tagctccgc tgctggnctt caacggggtt ntccgggtcat ttcctagcgc cggg 294

<210> 23

<211> 362

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttggg ttgttttat ttgtcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgctgatg aagacagaa 180
gctccggggt gacgaatttg gccgatggag nat gttttgg gggaacgccg ggactgagag 240
actccacggc agggcgaatt cccgtttggg gcttttttt tcttccctct ttttccctt 300
gcccttttg canccgngg agggagntgt tnaaggggag ggagggccag ccagtgtga 360
cc
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362

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```
ttccccagca ttcgagaaac tcctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaaact gcagcgcggt gagagagcga gagagaggga gagagagact ctccagcctg 120
ggaactataa ctctctgctg agaggcggag aactccttcc ccaaactctt tggggacttt 180
tctctcttta ccacctccg cccctgctgag gatttgaggg gccagttcgg ccgccgcgcg 240
cgtcttcccg ttccggcgtgt gcttgccccg gggaaccggg agggcccgcc gatcgcgccg 300
cgcccgccgc gagggtgtga gcgcgcgtgg gcgcccgccg agccgaggcc atggtgcagc 360
aaaccaacaa tgccgagaac acggaagcgc tgctggccgg cgagagctcg gactcggggc 420
ccggcctcga gctgggaate gcctcctccc ccacgcccgg ctccaccgcc t ccacggggc 480
gcaaggccga cgacccgagc tgggtcaaga ccccgagtgg gcacatcaag cgacccatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccagca 600
tgcaacaacg cgagatctcc aagcggctgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc ttctattcga gaggcggagc ggctgcgccct caagcacatg gctgactacc 720
ccgactacaa gtaccggccc aggaagaagg tgaagtccgg caacgccaac tccagctcct 780
cgcccgccgc ctctccaag ccgggggaga agggagacaa ggtcggtggc agtggcgggg 840
gcggccatgg gggcggcggc ggcggcgagg gcagcaacgc ggggggagga ggcggcggtg 900
cgagtggcgg cggcgccaac tccaaaccgg cgcagaaaaa gagctgcggc tccaaagtgg 960
cgggcggcgc gggcggtggg gttagcaaac cgcacgcaa gctcatcctg gcaggcggcg 1020
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ccgcgcctct gctgcccctg ggcccgcccg ccgaccacca ctgctgtg ac aaggcgcgga 1140
ctccagcgc ctccgctcc gcctcctcgg cagctcggc ctccgcagcg ctccggggcc 1200
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tgcgcgccgc ctgcgccgc ccgtccagcg cgccctcgca cgcgtcctc tcggcctcgt 1500
ccactcctc ctcttctcct tcctcgggct cctcgtcctc cgacgacgag ttccaagacg 1 560
acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
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cgctcgccgc gctcgaccgg gacctggatt ttaacttcga gcccggtccc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcaact actgaa gggc gcgcaggcag ggagaagggc 1800
cggggggggt aggagaggag aaaaaaaaag taaaaaaaag aaacgaaaag gacagacgaa 1860
gagttttaaag agaaaaggga aaaaagaaag aaaaagtaag cagggctcgt tcgcccgcgt 1920
tctcgtcgtc ggatcaagga gcgcggcggc gttttggacc cgcgctccca tccccacct 1980
tcccggggcg gggaccact ctgccagcc ggaggagcgc ggaggaggaa gagggtagac 2040
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ttcagatttg ctcccctttg cttgaagaga cccctcccc cttccaacga gcttcggac 2160
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cttcctgcat caccaccttg gttttgtttt attttgcttc ttggtcaaga aaggaggga 2280
gaaccagcg caccctctcc ccccttttt taaacgcgtg atgaagacag aaggctccg 2340
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gcaggcgaat tccggtttg ggcc ttttt tcttccctct tttcccttg cccctctgc 2460
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cgccggctgc tgggcctcg ctttctttc tacgtgaaat cagtggagt agacttcca 2700
gaccccgag gcgtggagga gaggagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtg ttcggaaaaa aaaaagaaa aaaaggg 2797

```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5 (RNF5) gene.

<400> 25

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acgggggccc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgtg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtccgc ttatgggcg agggagccag aagccccagg 240
atcccagatt aaaaactcca ccccgcccc aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatittgtg ataccgggg cttccaactn ttcatttggg gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

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atggcagcag cggaggagga ggacggggc cccgaaggc caaatcgca gcggggcggg 60
gcgggcgcga cttcgaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

```

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gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgaggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg cccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
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catgagcctt tccgccgggg tacagggtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttcct gtttctcgcc atcttcttct ttttttggct gctcagtatt 540
tga 543

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

gccgtggggg gggaaagtgg gaag gtggag ttttccccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggagggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gntccagca ggatggacct cagccgcagt naggcagcta caggaatcct taggggtctg 240
ctgggttggg gggtcagetc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatntn acatagagga tttcgtcagg ctctggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgtatgtt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccaggga atcgctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcgagg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agatttttgg gagnacacac ttttaagggc tttncctt 418

<210> 29

<211> 5015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

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gagtgagggt ctggaggaat gtttaccaga cacagagccc agagggacag cgcccagagc 60
ccagatagag agacacggcc tcaactggctc agcaccaggg tccccttccc cctcctcagc 120
tccctcctctg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggt gcccttggtc ctggcctggt gggcggaggc aaagggggag ccagggcgcg 240
agaaagggtt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggt 300
gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcctaaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cggcccgtct cccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag ttggcacc cc atggcgctggc ggtgccccag 480
gatgggcagg gtcccgctgg cctggtgctt ggcgctgtgc ggtggggcgt gcatggcccc 540
caggggcacg caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacaggtgc 600
ccggggactc acgggcaccc ttccgtgtca gctccagggt caggagagc ccccgagggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccaga cccaggtgcc 720
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```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)
gene.

<400> 30

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gaatggcaca cctactggc tgg ttgcaa ctctggaa actgactggg gtgacaatgg 120
cttctttaaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggcc tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttatc ttttaagtca cgttaaggat 300
acaagtttc agacaggggc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttccaaggg gaggaccaag ttctggggct aacattcccc agcctnttgg ttttaacagtt 420
gncaggacag ggcctgtt 439

```

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<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
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tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980
ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

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aacaacaga aaaaagaag aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgcccag 240
cctccgtctg aggggaagatg ggcagagtca cagtgggtgc gaggggcccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggcttncca cattttccca cagcggtaga 480
agttagtttt tg                                     492
```

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

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ctggcactta aggttcgcta tcttgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggtcta tggcttctac gatgagtgc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg cacggggggc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt                                     330
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<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagagggtgg 240
actcgccagt cacagtgtgc ggcgacatcc atggacaatt ctatgacctc aaagagctgt 300
tcagagtagg tggcgacgtc cctgagacca actacctctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaaggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```


22/292

```

totacgatga gtgcctgcgc aagtaagggt cgggtgactgt gtggcgctac tgcactgaga 540
tctttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
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ggggcggtgag cccccgagga gccggctacc tatttggcag tgacgtggtg gccagttca 780
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429

```

<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)
gene.

<400> 35

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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaat gacctgaaga 240
gtcctgttta antttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcttac ccaggaccn ttcccacctc actagggnac ttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggncac tcccngttg gatgggtntt gggggaggag nctgntggg 480
gntttttccc at 493

```

<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

<400> 36

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tttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgtgg ggcagcagca 120

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gcagggggag gnttggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaagggca aggggcacgg ccttngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

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ggcagcagcg ccctcccaga ggcctacctt caagcagctg gtggaggcgc tggacaagg 120
ctgctggccg tctctgagga gtacctcgac ctccgctga ccttcggacc ctattcccc 180
tctggtggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctcttccct ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

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gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120
agtccagctt gggtcctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
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```

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gctgactttg ggctggcccg cggcgtccac cacattgact actataagaa aaccagcaac 2100
ggccgcctgc ctgtgaagtg gatggcggc gaggcctgt ttgaccgggt gtacacacac 2160
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ctcgaccttg atagcatgg gccctggc cagagttgct gtgccgtgct caagggccgt 2700
gcccttggc ttggagctg cgtgcctgtg tccgtatggc ccaaatgtca gggttctgct 2760
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cctttcccca cacctcccc tgctgctgct gcccagcgt cttgacggga gcattggccc 2940
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tttttttgaa ataaa

```

3015

<210> 39
 <211> 252
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(252)
 <223> 3' terminal sequence. ectonucleotide
 pyrophosphatase/phosphodiesterase 2 (autotaxin)
 (ENPP2) gene.

```

<400> 39
gtgtgattta ttatgtttaa gattggttta taaggottaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgtt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata tttcctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta

```

252

<210> 40
 <211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

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ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaaga atatgcttcg 60
gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtnctgt gacctttgna cc 382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
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ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgt atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggtgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgtct ccatgacttt gatgagctgt gtttgaagac agcccgctgc 300
tgaggagtga ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtgtt ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaagg cttgtggcac acactctccc 600
tacctgagga cgggtgaccc aactaaaacc tttcctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgacctgt atttgatgcc 720
acttttcatc tgcgagggcg agagaaatth aatcatagat ggtggggagg tcaaccgcta 780
tggtattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgcac 840
cctcagcagc ggagaatatt aaccatattg cagtggctca ccctgccaga tcatgagagg 900
ccttcggtct atgccttcta ttctgagcaa cctgatttct ctggacacaa atatggccct 960
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ggaatggaag atgtcacatg tgatagaact gagttcttga gtaattacct aactaatgtg 1140
gatgatatta ctttagtgcc tggaaactcta ggaagaattc gatccaaatt tagcaacaat 1200
gctaaaatag accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgccaa caacagaaga 1320
```

26/292

```
attgaggata tccatttatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
gtttataaga aaccatcagg aaaatgcttt ttccaggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttgttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
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cgacctgcag tgctttatcg gactagatat gatattttat atcacactga ctttgaaagt 1860
ggttatagtg aaatattcct aatgccactc tggacatcat atactgtttc caaacaggct 1920
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ccgagtttca gt cagaactg tttggcctac aaaaatgata agcagatgtc ctacggattc 2040
ctctttcctc cttatctgag ctcttcacca gaggtctaat atgatgcatt ccttgtaacc 2100
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tatgactatg atggcttaca tgacacagaa gacaaaataa aacagtacgt ggaaggcagt 2280
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gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg acactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592
```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```
acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
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cctactatta aggcaattga gaagaggag agcaaggag tccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcn tggntttcct tcagccatgg ttgagcaagg 240
aaagagcccg cagagacctc ttagggcag gaaggccagc ccctcaaagc ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctggggcgct tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467
```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

27/292

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3 (p65))
(RELA) gene.

<400> 43

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ggcagcaggc ggggccgggt cgcagctggg cccgcggcat ggacgaactg ttccccctca 60
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gctccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggtc a ccaaggacc 240
ctctcaccg gcctcaccgc cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccgagc cgctgcatcc acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaacccct 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggtctgtct 480
tccaggtgac agtgcgggac ccacaggga ggccccctcg cctgccgcct gtcctttctc 540
atcccatctt tgacaatcgt gcccccaaca ctgccgagct caagatctgc cgagtgaacc 600
gaaactcttg cagctgcctc ggtggggatg agatcttctt actgtgtgac aaggtgcaga 660
aagaggacat tgaggtgtat ttcacgggac caggctggga ggccccaggc tccttttctc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac ccctccctac gcagacccca 780
gcctgcaggc tcctgtgcgt gtctccatgc agctgcggcg gccttccgac cgggagctca 840
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aacgtaaaag gacatatgag accttcaaga gcatcatgaa gaagagtcct ttcagcggac 960
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caggaggcat agtttttagt gaacaatcaa agcacttgga ctcttgctct ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
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<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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aactctttcc tttggttggtg ctaagagggtg atgcccgaag tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaaactt taaagtccgc ttcttttggt taaccaaagc cagcctgg ca 180
tactttgaag atcgatcatgg gaagaagcgc acgctgaagg ggtccattga gctctccga 240
attcaaatgt gttgaggttg tgaagaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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aatatattca acacttacaa aaagtatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttaca gtaacatcac aaatgctcac 240
atcttcacat gctcttaaag tattatttgt actcagtgta aggcatttat cgtttttcat 300
acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaagttg ccgcttccca gcattaagac atgcacccac ccctcttcta agattttcta 420
aacttgtatt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat tttaaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaata gtgtagcaa atatcattct ctacagctac cttaagtaaa agacaaaaca 660
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gaggtgatgc ccaaggtgca ccaccttca agaactggat catgaacaac tttatcctcc 2040
```

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30/292

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 ctgtacagcc tgacactgta tgggtgcgga ggacccaca agggcgacag catccaggga 11580
 accgccccga ccctcagccc agttctggag agccccctg acctccaatt cagtgaatc 11640

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```

aggagacct cagccaaggt caactggatg cccccaccat cccgggcgga cagcttcaaa 11700
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gtaccg

```

<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating
factor 1 (macrophage) (CSF1) gene.

<400> 48

```

ttttgcagct tgtgcacttc ttttattatt aaatatataa gcagcttccct atctttttaa 60
tagatattta aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttccattttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttcact

```

438

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

```
ggcacgaggg gagctctgac tgaagatggg cctttgaaat ataggtatgc acctgaggtt 60
gggggaggggt ctgcactccc aaaccccagc gcagtgtcct ttccctgc tg ccgacagaaac 120
ctggggctga gcaggttatc cctgtcagga gccctgggac tgggctgcat ctacagcccca 180
cctggcatgg tatccagctc ccattcactt cttcaccctt ctttcctcct gaccttgggt 240
caacagtgat ggaccttcca actcttcacc caccctctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagc                                     390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) .
(CSF1) gene.

<400> 50

```
agccgctctc cgcattcccag gacagcgggtg cggccctcgg ccggggcgcc cactccgcag 60
caccacagca gcgagcgagc gagcgagggc ggccgacgcg cccggccggg acccagctgc 120
ccgtatgacc gcgcccggcg ccgcccggcg ctgccctccc acgacatggc tgggctccct 180
gctgttgttg gtctgtctoc tggcgagcag gagtatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggctgattg acagtcagat 300
ggagacctcg tgccaaatta catttgagtt tgtagaccag gaacagttga aagatccagt 36 0
gtgctacctt aagaaggcat ttctcctggt acaagacata atggaggaca ccattgcgctt 420
cagagataac accccaatg ccattcgccat tgtgcagctg caggaactct ctttgaggct 480
gaagagctgc ttaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
tgagacacct ctccagttgc tggagaaggc caagaatgtc tttaatgaaa caaagaatct 600
ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagctttg ctgaatgctc 660
cagccaagat gtggtgacca agcctgattg caactgcctg taccccaag ccattccctag 720
cagtgaaccg gcctctgtct cccctcatca gcccctcgcc ccctccatgg cccctgtggc 780
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acatgagagg cagtccagg gatcctccag cccgcagctc caggagtctg tcttcacct 1620
gctggtgccc agtgtcatcc tggctctgct ggccgtcggg ggcctcttg t tctacaggtg 1680
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```

gaggcgggcg agccatcaag agcctcagag agcggattct cccttgagc aaccagagg 1740
cagccccctc actcaggatg acagacaggt ggaactgccg gtgtagaggg aattctaaga 1800
cccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
cccggacaca gtactccaga tgttgtctga ccagctcaga gagagtacag tgggactgtt 1920
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gttcatttc ccataaactt ctgtcaagcc agaccatctc taccctgtac ttggacaact 21 00
taactttttt aaccaaagtg cagtttatgt tcacctttgt taaagccacc ttgtggttc 2160
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gatgtagctg tgacctatt gttcctcacc cctgccc ccc gccaaccca gctggcccac 2340
ctcttcccc tcccaccaa gccacagcc agccatcag gaagccttc tggcttctcc 2400
acaaccttct gactgtctt tcagtcatgc cccctgctct tttgtattg gctaatagta 2460
tatcaatttg cactt                                     2475

```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```

atcngttgaa tagttgattc catacatttc cagg tcttga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactggctc ctggttaagtt tgtgtggtc catcactctt tgagggatca nccgctcaga 180
gctgaggtag ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcctc gctaagggat 300
tcttttctt cacttnggag ggaggaaaag tttctggggt gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc                                     397

```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

```

ggacgaggca gggcgggcg ggcctctaag ggtctgtctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtggtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagtta ccaccatgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttcaa 360

```

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gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

aggcagggcg ggcgggcgct ctaagggttc tgctctgact ccaggttggg acagcgtctt 60
cgctgctgct ggatagtcgt gttttcgggg atcgaggata ctaccagaa accgaaaatg 120
ccgaaaccaa tcaatgtccg agttaccacc atggatgcag agctggagtt tgcaatccag 180
ccaaatacaa ctggaataca gctttttgat caggttgtaa agactatcgg cctccgggaa 240
gtgtggtact ttggcctcca ctatgtggat aataaaggat ttctacctg gctgaagc tg 300
gataagaagg tgtctgccca ggaggtcagg aaggagaatc cctccagtt caagttccgg 360
gccaaagtct accctgaaga tgtggctgag gagctcatcc aggacatcac ccagaaactt 420
ttcttcctcc aagtgaagga aggaatcctt agcgatgaga tctactgcc ccctgagact 480
gccgtgctct tggggctcta cgctgtgcag gccaaag tttg gggactacaa caaagaagtg 540
cacaagtctg ggtaccctcag ctctgagcgg ctgattccctc aaagagtgtat ggaccagcac 600
aaacttacca gggaccagtg ggaggaccgg atccaggtgt ggcatgcgga acaccgtggg 660
atgctcaaag ataagtctat gttggaatac ctgaagattg ctgaggacct ggaaatgtat 720
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aacattagtt ttaaaaaggg aaagttttgt tctgtatatt ttgttacctt ttacagaata 2640
aaagaattac atatgaaaaa ccctctaaac catggcactt gatgtga tgt ggcaggaggg 2700
nagtgggtga gctggacctg cctgctgcag ctgcagtcac gtgtaaacag gattattatt 2760
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gccactcat tccttctcgt gcactgcttt ctcttcaca gctaagatgc catgtgcagg 3000
tggtatccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa 3064

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 54

tgcataaata ccaatttttc cctgatgtaa gtttagtcag ttataatct agaaatgatt 60
gataacagca atatatcata ttttctatct gtagtggtca ttattttaag acaagcaata 120
attaaaggaa gttgggatgg gatgctactt taaatacatg taaaacatac tgtacaaaca 180
tacttggctt tactattttt ttctaacca tcaagagtgc ctcccaaat aa gnccagtg 240
aagacaaagt atactatcaa atatgggctt ccnggaacaa aaaccctctt aacaaggnt 300
ccaaacccta ttaccacaaa tttcccggt cttttaagggt ttccatttgg aaaccacaaat 360
gtctatatgg ccggttggtg attancatgg ggnntttctt ggnnttcctt cttccncct 420
ctttttaacc ggtgg 435

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 55

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tggtgctgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
tggttggtg agaattgagg actgtcccat taacaatcct agatctggaa gatctccac 180
aggtaatact ccccggtgga ttg acagtgt ttacagaaaag gcaaatccaa acattaaaga 240
ttcaaaagat aatcagggca aaacaaaatg tggggaatn ggcagtgtc ccatgncgta 300
ccgtggggtt tnggaaaatc gcctggaact cttttatttc aggtgggatg cccctgacca 360
aaaaggganc tttnggttna aaccggggnc aaattattcc tgttccctgt tttc 414

<210> 56

<211> 10383
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(10383)
<223> adenomatosis polyposis coli (APC) gene.

<400> 56
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agttgttaaa gcaagttgag gcaactgaaga tggagaactc aaatcttcga caagagctag 120
aagataattc caatcatctt acaaaactgg aaactgaggg atctaataatg aaggaagtac 180
ttaaacaact acaaggaggt attgaagatg aagctatggc ttcttctgga cagattgatt 240
tattagagcg tcttaaagag cttaacttag atagcagtaa tttccctgga gtaaaactgc 300
ggcacaataa gtccctccgt tcttatggaa gccgggaagg atctgtatca agccgttctg 360
gagagtgcag tcctgttctt atgggttcat ttccaagaag agggtttgta aatggaagca 420
gagaaagtac tggatattta gaagaacttg agaaagagag gtcattgctt cttgc tgata 480
ttgacaaaaga agaaaaggaa aaagactggg attacgctca acttcagaat ctactaaaa 540
gaatagatag tcttccttta actgaaaatt tttccttaca aacagatatg accagaaggc 600
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<210> 57

<211> 404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(404)

<223> 5' terminal sequence. mucin 1, transmembrane
(MUC1) gene.

<400> 57

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catttccttt ctctgccag tctggggctg ggggtgccagg ctggggcacc gcgtgctgg 120
tgctggtctg tgttctggtt gcgctggcca ttgtctatct cattgccttg gctgtctgtc 180
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ctatgagcga gtacccacc taccacacc atggggcgct atgtgcccc taggcagtac 300
cgatcgtagc ccctatgaga aggtttttng caggtaatng gttggcagca gcttttttta 360
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<210> 58

<211> 1721

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1721)

<223> mucin 1, transmembrane (MUC1) gene.

<400> 58

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agaagttcag tgcccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240
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<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 59

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<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 60

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ttccttgtag cttntntntt gaaccacgga gttttncttn aggtttccat tccngaaaa t 360
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<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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tgatttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

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<210> 63

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(457)

<223> 5' terminal sequence. egf-like module
 containing, mucin-like, hormone receptor-like
 sequence 1 (EMR1) gene.

<400> 63

tctgtcaac ggccaggtac gagaagaata caagaggtgg atcactggga agacgaagcc 60
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 gggttaaagt cttttcttgc tttcaaatat gctatggagc cacagttgag gacagtagtt 180
 tcctgcagga gcctaccctg aaatctcttc tcag cttaac atgggaaatg aggatccac 240
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 tgcantgatg gaggaaatca ggtgtttttt gntccaaacg gaccatttta ntctttcgtg 360
 gntttgcaan ttttttcaan ttccagagtt ttttgaggna caggacccaa nttcantggg 420
 catgnaccag gaacatcggg gttaaccont tttgttt 457

<210> 64

<211> 3149

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3149)

<223> egf-like module containing, mucin-like,
 hormone receptor-like sequence 1 (EMR1) gene.

<400> 64

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 caaacacaaa gggtaataac ttagagaga gtaccttgTc ccagcttat gccacctgca 180
 ccaatacggT ggacagttac tattgcactt gcaaacaagg cttcctgtcc agcaatgggc 240
 aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300
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gcctgacaca gagaacctct caataaatga tttgtgcct gtctgactga tttaccctaa 3120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

```

<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

```

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tgaaggttta cagactgggtc aagggaaggac gaacagagag aatggggctc gaggggtcac 120
atcccgtgga ggggtggcggg gtccttggtc tgcgtgtggg gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaagacca ccaggccttg gggagcaggg ctttggcaag 240
caggccgcct cgga gaaaaa caatgactaa ctcatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

```

ccccggggcgn aggggngaaa gcaattncaa agcctttagg aaatttcaat tt

412

<210> 66

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 5' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 66

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tatggaagga aaacgttaag actatttttt ttttaaagaa acaacagtca agcctaaaaat 120
ttgagacccc gaggcagctt cccgagggag actgctcaga caggaactgc aggacagaag 180
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ggcggttcca gccatcttga tgttgatcc ngttttcagt nttccccant tgcctnttca 420
gggatngagt tagttcattt tt 442

<210> 67

<211> 5737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5737)

<223> k1aa0427 gene product (K1AA0427) gene.

<400> 67

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gatccctcc gcagctggga cgctccgaac tcgaggcagg agtcggctct ccggagcctc 180
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<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

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tctttttaa gctcaaaac atttttattg tcaggaaagc ttttcagtgg ccagggatca 120
gtctcatggc cgtagaagca gccaaattcc tctgcctttg ccttccttc aggagtca ca 180
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gccactctgc aatgtccctg ggnccgatg aggtaacaaa tgcaccccg ggaccagag 300
gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377
```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

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gaataatctc aagaatcaaa tcatactcct tccaaagcc tggccacaga aagtcctccc 120
ctgcccagg gaaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgcagga caaagggcc cca gaggagg aagccctacc cntgggacac 240
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50/292

agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

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actttccaaa gcactg cgtg ctgatgaaaa ctactacaag gccagaccc atggaaagt 1680
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ggccatgaga ctgatccctg gccactgaaa agctttcctg aca ataaaaa tgttttgagg 2520
ctttaaaaaa aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaatgtga gtttcaatcc tgaaagtttc 60
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ctgcaagata cgtttcctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
ggagattcat ccctcacatg cctgggctng ggaatgttca gtgcattgtga cgccctatt 300
tttctccttt t 312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctaggtaca acttttggca tgggt tttttc 60
tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
ttcactgacc tgtgcttttg aggaccaga tgtaacacc accaatctgg aatttgaaat 240
atgtggggcc ctgctggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgaga 360
aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggctccttt 420
tgacctgagt gtcattctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc 480
acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa 540
ggatgaaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tcctgcagag 600
aaagctcaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt 660
taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
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cgctctgttg gtcacttttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg 840
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tttaaatgtg agtttcaatc ctgaaagttt c ctggactgc cagattcata ggttgatga 960
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tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttgga ctacaaacag 1260
cacgctgccc cctccatttt ctctccaatc tggaaatcctg acattgaacc cagttgctca 1320

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```

gggtcagccc attcttactt ccctgggac aaatcaagaa gaagca tatg tcaccatgtc 1380
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aagatgattt aaaagggaag tctagagttc ctagtctccc tcacagcaca gagaagacaa 1500
aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtc agagcatcct gcttctacca tgtggatttg 1620
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<210> 73
 <211> 236
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(236)
 <223> 3' terminal sequence. v-myc avian
 myelocytomatosis viral oncogene homolog (MYC)
 gene.

```

<400> 73
taaaaaaat agaaaaaat caactttaaa aagcaaaatg tacttaata aaaaaaatta 60
gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt tttattaaag ttattttacat ttaatgggca atatttacag aggaacatt 180
gtgtaaatct taaaattttt taaaanccaa ttcttaata ccaaactctgt taaggg 236

```

<210> 74
 <211> 413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(413)
 <223> 5' terminal sequence. v-myc avian
 myelocytomatosis viral oncogene homolog (MYC)
 gene.

```

<400> 74
acgtctccac acatcagcac aactacgcag cgcctccctc cactcggaag gactatcctg 60
ctgccaagag ggtcaagttg gacagtgtca gagtcctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgaggag gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atccggaggt tgggaaaaca atgaaaaggc cccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggaggagacc aaaagttcat tttnttgaag 360
gagggnnttt ttttccgggn aacgacgagg aaccattttt aaacacaant ttt 413

```

<210> 75
 <211> 2121
 <212> DNA/RNA
 <213> Artificial Sequence

<220>

53/292

<223> Description of Artificial Seq uence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

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ataaaagccg gttttcgggg ctttatctaa ctcgctgtag taattccagc gagaggcaga 180
gggagcgagc gggcggccgg ctaggggtga agagccgggc gagcagagct gcgctgcggg 240
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cttgatcccc caggcca gcg gtccgcaacc cttgccgat ccacgaaact ttgcccatag 360
cagcggcgcg gcacttttca ctggaactta caacaccga gcaaggacgc gactctccc 420
acgcggggag gctattctgc ccatttgggg aacttcccc gccgctgcca ggaccgctt 480
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cagcagcaga gcgagctgca gccccggcgc ccagcagagg atatctggaa gaaattcgag 720
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tctgaagagg acttgttgcg gaaacgacga gaacagttga aa cacaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg ttcaaagtgc atgatcaaat gcaacctcac aaccttggct 1980
gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttat gct taccatcttt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
```

<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata -binding protein 3
(GATA3) gene.

54/292

<400> 76

tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
gggggtccaga ttcagtgggt ggaacacaga caccacagt agtcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggctctt 260

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 77

cattctgggt catagatggc atcttttcac tgtgttctca cattgggtga aaggaagaac 60
tctggtttct tcacttcctt ataaggcac caatcttatt cagagggct tcaccctga 120
aataatcacg tctcaaaaac cccaccttc taatattcta ataccatcac gtgagggctt 180
aggtttcaac ataagaattc ggtggtggtt ggggttnggg gagagggaaa caaacatcca 240
gaccagaac cgaaaaatgt ctacgaaatc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctnctgtt taaccggggc cgccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc ttnaggccan tccaggga 409

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

tccagcctt cccatcccc caccgaaagc aaatcattca acgaccccc accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tccccgcgcg ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
ggtgagccac caccaccccg ccgtgctcaa cgggcagcac ccggacacgc accaccggg 240
cctcagccac tctacatgg acgcggcgca gtaccgctg ccggaggagg tggatgtgct 300
ttttaacatg gacggtcaag gcaaccacgt cccgccctac ta cggaaact cggtcagggc 360
cacggtgcag aggtaccctc cgaccacca cgggagccag gtgtgccgc cgcctctgct 420
tcattggtcc ctaccctggc tggacggcgg caaagccctg ggcagccacc acaccgcctc 480
cccctggaat ctacgccct tctccaagac gtccatccac cacggctccc cggggcccct 540
ctccgtctac ccccgggcct cgtcctctc cttgtcgggg ggccacgcca gcccgcacct 600
cttcacctc ccgccaccc cgccgaagga cgtctcccc gaccatcgc tgtccacccc 660
aggtcgggcc ggctcggccc ggcaggacga gaaagagtgc ctcaagtacc aggtgcccct 720
gcccgacagc atgaagctgg agtcgtccca ctcccgtagc agcatgacc ccctgggtgg 78 0
agcctcctcg tcgaccacc acccatcac cacctaccg ccctacgtgc ccgagtacag 840
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cctctgcaaa ggaatatacca gttctgggca atcagtgtta cc gttcacca gttgccattg 2100
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ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttcct 2280
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cattcagttg gcaaaaaaaa aaaaa 2365
```

<210> 79
<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(328)
<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

```
<400> 79
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ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgcctt agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggag 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgctccc 300
tgtggccgat cccanagtcc actnggat 328
```

<210> 80
<211> 428
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(428)

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<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

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ggctcccccac ccttgagaag tgcctcagat aataccctgg tggccatgga cttctctggc 60
catgctgggc gtgtcattga gaacccccgg gaggtcttga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctacgcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggtc tngtagacgg cctgttcttg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatttt aagcattggt 42 0
tgattggc 428
```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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cacagggctc cccccgcct ctgacttctc tgtccgaagt cgggacaccc tctaccacc 60
tgtagagaag cgggagtggg tctgaaataa aatccaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgtctggg ctctctcagg acaagggca c 180
acaactggtt cgttaaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
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ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcacc 360
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cccaaccctt tccctgagct ctgcagtcct cctcacaga gcccaattct cggggggccc 480
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tgccaccccc acctagcact ggagcggggt ttgaggagacc acgagtcctg ggtggaagtg 720
cagggtgcct ggcccgtggg cggagatagc cgcttctgtc tccggaaaaa cttcgccaag 780
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gccgcgcgcc cctccacca tccagtggac tctggggcgc ggccacaggg gacgggatga 1 920
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tgggggcagc ccaggcggtt tcacgccccca cacttt gtac agaccgagag gccagttgat 2160
ctgctctgtt ttatactagt gacaataaag attatTTTT gatac 2205

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
acagacagat aaagttccaa gtaaaacggg agctgctaaa aagggtatgt acttatattt 120
gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
actatttgca tttttttatc ataaaacaat taagggaagta taagtgccta taaggaggac 240
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300
gttgtanttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
gene.

<400> 83

atggccaagt cgggtggctg cggcgcggga gccggcggtg gccggcgcaa cggggcactg 60
acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccaacaa aaatgattct 120
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
cttcgtcctg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
gatgaagatg taggaatgaa ttgcaggag gttaccttg tgccaggttt atacaagatc 300
tttgatgaaa ttttgggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
attaaagttt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
attccagtag tagaacacaa ggtagagaaa gtttat gtic ctgctttaat ttttggacag 480
cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacagggtg tcgtaatggg 540
tatggtgcaa aactttgtaa tatttcoagt acaaagttaa cagtagaaac agcttgcaa 600
gaatacaaac acagttttta gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
aaaatttaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
aaatttaaga tggaaaaact tgacaaggat attgtggccc tcatgactag aagggcata 780
gatttggctg gttcgtgtag aggggtcaag gtcatgttta atggaaagaa attgcctgta 840
aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

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gaaaaaggat tccagcaaat cagctttgta aatagtattg caactacaaa aggtggacgg 1020
 cacgtggatt atgtggtaga tcaagttggt ggtaaaactga ttgaagtagt taagaaaaag 1080
 aacaaagctg gtgtatcagt gaaaccattt ca agtaaaaa accatatatg ggtttttatt 1140
 aattgcctta ttgaaaatcc aacttttgat tctcagacta aggaaaacat gactctgcag 1200
 cccaaaagtt ttgggtctaa atgccagctg tcagaaaaat tttttaagc agcctctaat 1260
 tgtggcattg tagaaaagtat cctgaactgg gtgaaattta aggtcagac tcagctgaat 1320
 aagaagtgtt catcagtaaa atacagtaaa atcaaaggta ttcccaaact ggatgatgct 1380
 aatgatgctg gtggtaaaca ttccctggag tgtacactga tattaacaga gggagactct 1440
 gccaaatcac tggctgtgtc tggattaggt gtgattggac gagacagata cggagttttt 1500
 ccactcaggg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaat 1560
 gctgaaataa ataataattat taaaatagtt ggtctacaat ataagaaaag ttacgatgat 1620
 gcagaatctc tgaaaacctt acgctatgga aagattatga ttatgaccga tcaggatcaa 1680
 gatggttctc acataaagg cctgcttatt aatttcatcc atcacaattg gccatcactt 1740
 ttgaagcatg gtttctctga agagttcatt actcctattg taaaggcaag caaaaataag 1800
 caggaaactt ccttctacag tattcctgaa tttgacgaat ggaaaaaaca tatagaaaac 1860
 cagaaagcct ggaaaaataa gtactataaa ggattgggta ctagtacagc taaagaagca 1920
 aaggaatatt ttgctgatat ggaaaggcat cgcactttgt ttagatatgc tggctcctgaa 1980
 gatgatgctg ccattacctt ggcatttagt aagaagaaga ttgatgacag aaaagaatgg 2040
 ttaacaaatt ttatggaaga ccggagacag cgtaggctac atggcttacc agagcaattt 2100
 ttatagtgtg ctgcaacaaa gcatttgact tataatgatt tcatcaacaa ggaattgatt 2160
 ctcttctcaa actcagacaa tgaaagatct atac catctc ttgttgatgg ctttaaacct 2220
 ggccagcgga aagttttatt tacctgtttc aagaggaatg ataaacgtga agtaaaagtt 2280
 gccagttgg ctggctctgt tgctgagatg tcggcttctc atcatggaga acaagcattg 2340
 atgatgacta ttgtgaattt ggctcagaac tttgtgggaa gtaacaacat taacttgctt 2400
 cagcctattg gtcagtttgg aactcggctt catgggtggca aagatgctgc aagccctcgt 2460
 tatattttca caatgttaag cactttagca aggtactttt ttctgtctgt ggatgacaac 2520
 ctctttaatg tcctttatga tgataatcaa cgtgtagagc ctgagtggta tattcctata 2580
 attcccatgg ttttaataaa tgggtctgag ggcattggta ctggatgg gc ttgtaaaacta 2640
 cccaactatg atgctagga aattgtgaac aatgtcagac gaatgctaga tggcctggat 2700
 cctcatcca tgcttccaaa ctacaaaaac tttaaaggca cgattcaaga acttggtaa 2760
 aaccagtatg cagtcagtg tgaaatattt gtagtggaca gaaacacagt agaaattaca 2820
 gagcttcag ttagaacttg ga cacaggtg tataaagaac aggttttaga acctatgcta 2880
 aatggaacag ataaaacacc agcatthaatt tctgattata aagaatatca tactgacaca 2940
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 catatgggat gtctgaagaa atatgaaact gtgcaagaca ttctgaaaga attctttgat 3120
 ttacgattaa gttattacgg tttacgtaag gagtggcttg tgggaatgtt gggagcagaa 3180
 tctacaaagc ttaacaatca agcccgtttc atttttagaga agatacaagg gaaaattact 3240
 atagagaata ggtcaaagaa agatttgatt caaatg ttag tccagagagg ttatgaatct 3300
 gaccagtgaa aagcctggaa agaagcaca gaaaaggcag cagaagagga tgaaacacaa 3360
 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaga ttttaattat 3420
 attttaaata tgtctctgtg gtctcttact aaagaaaaag ttgaagaact gattaaacag 3480
 agagatgcaa aagggcgaga ggtcaatgat cttaaaagaa aatctccttc agatctttgg 3540
 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaaatctca agaacgagaa 3600
 gatgttctgt ctggaatgtc tggaaaagca attaaaggta aagttggcaa acctaagggtg 3660
 aagaaactcc agttggaaga gacaatgcc tcaccttatg gcagaagaat aattcctgaa 3720
 attacagcta tgaaggcaga tgccagcaaa aagttgctga agaagaagaa gggatgatt 3780
 gatactgcag cagtaaaagt ggaatttgat gaagaattca gtggagcacc agtagaagg 3840
 gcaggagaag aggcattgac tccatcagtt cctataaata aaggtcccaa acctaagagg 3900
 gagaagaagg agcctggtac caga gtgaga aaaacaccta catcatctgg taaacctagt 3960
 gcaaagaaag tgaagaaacg gaatccttgg tcagatgatg aatccaagtc agaaagtgat 4020
 ttggaagaaa cagaacctgt ggttattcca agagattctt tgcttaggag agcagcagcc 4080
 gaagaaacctc atatacatt tgatttctca gaagaagagg atgatgatgc tgatgatgat 414 0
 gatgatgaca ataattgatt agaggaattg aaaggtaaag catctcccat aacaaatgat 4200
 ggggaagatg aatttgttcc ttcagatggg ttagataaag atgaatatac attttacca 4260
 ggcaaatcaa aagccactcc agaaaaatct ttgcatgaca aaaaaagtca ggattttgga 4320
 aatctcttct catttcttcc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgtttt tcaccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacggg agctgctaaa aagggaac cgtcttcaga tacagtccct 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaaact tgactcggat 4560
 tcagaatttg gcattccaaa gaagactaca acaccaaaag gtaaaaggccg aggggcaag 4620

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```
aaaaggaaag catctggctc tgaaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttccctcag acttcctac tgagccacct tctctgccac gaaccggctc g gctaggaaa 4800
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa                                         4866
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<210> 84
<211> 311
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(311)
<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

```
<400> 84
cacttttatt gaaatacaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggtc ggctgcttgg ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatata ttgtcatgga cagtcgttct atgggtgggca tttgagcttt ggcccttgga 180
gtttcaaatg attgctgtac cttccgaaat acttctcta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t                                         311
```

<210> 85
<211> 1291
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1291)
<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

```
<400> 85
gctctttcca acgtgttaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggt ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaatctaca gatgccctca 360
agctttgtcc tcatgaagaa ttctgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaaagg gagaaacaac cgcacacgcc tggtctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggctctga ctatagtgtg gatgtagaag agaacttgac agccagggat atggagtcag 600
cgctgagggc atttgtctac agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gaggaatct gcggaactgt gcatgatgag aaaaaaccag 720
atgtgtctgt ttatgacacc atcttcacga tattcaacaa ccgcaactgc ctgagcttga 780
aggacaaacc caaggtcatc attgtccagg cctgcagagg tgcaaaccgt ggggaactgt 840
gggtcagaga ctctccagca tccttgaag tggcctcttc acagtcattc gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960
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```

cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtac 1080
agcaatcatt tgaactcca agggccaaag ctcaaagcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaa a 1291

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<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 86

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tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggctgtg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaacn ccgcg ccgcg tnnccacgca 180
caggagcctt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga cccagtcctt ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319

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<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 87

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cgcagcaaac acatccgtag aaggcagcgc ggccgccga g agccgcagcg ccgctcgccc 60
gccgcccccc acccgcgcgc cccgcccggc gaattgcgcc ccgcgcccct cccctcgcg 120
ccccgagaca aagaggagag aaagtttgcg cggccgagcg gggcaggtga ggagggtgag 180
ccgcgcggga ggggcccgcg tcggcccggg ctacgcccc gccgcgccc ccagcccgcg 240
gccgcgagca gcgcccgg ac ccccagcgg cggcccgcgc ccgcccagcc cccgggccc 300
ccatggggcg cgcgcccgc accctgcggc tggcgctcg cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgcc tgcagctgct cccgggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgg tcagtgcgaa ggaagtggac tctggaaacg 480
acatttatgg caacctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaagatatata gagtttatct acacggcccc ctctcgga gtgtgtgggg 600
tctcgctgga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
gcaagatgca catcaccctc tgtgacttca tcgtgccc tg ggacaccctg agcaccaccc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgtacatc tctccccgg acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900

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cctgtgcgtg gtaccgcggc ggggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctgggtccagc tctgacatcc cttcctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d-dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta ttctcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcat gggggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180
ccaatcataa aaaagtcatg accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d-dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcgggn tngagaaaac 60
gactctgcgc cgccgtgcc tccatcctgg gcaaacctgc ggaccgcgtg aacgtgacgg 120
tacggccggg cctggccatg gcgctgagcg ggtccaccga gcctgcgcg cagtgttcca 180
tctcctccat cggcgtagtg gggcaccgcg agggacaacc gcagccacag cgcccatctc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90
gatcccggtg ccagggaccc tgcccagttc caggcgtcgc ctaaccaga aacgactggg 60
cgccggtcc tggaaaggcc ccagcgacg gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg 240
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctctccat cggcgtagt ggacccgagg aggacaaccg cagccacagc 360
gccacttct ttgagtttct caccaaggag ctaccctgg gcc aggaccg gatacttacc 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacgggtcat gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcatg caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaataa atgaagagag ctctctcatt 660
caaaaa 666

<210> 91
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91
gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgtgtgg atgattcggg 180
cacttcaggg agcttgagga taattgtcga ttttatgtga atccctgcgt aggcaatggg 240
agagggtata ataaggcagg aaaggcgag actcttcac agccatctgc aggggatggg 300
aagtccccga ccagacagg gtagatctca tttcttttg gttttcaggg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt 443

<210> 92
<211> 243
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(243)
<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92
gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcttgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctcc tgctgctgct ggggtgttcaa 180
acctgctcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat 243

<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
aaacatgaac atcaaaggat cgccatggaa agggctccctc ctgctgctgc tgggtgtcaaa 60
cctgctgctg tgccagagcg tggcccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccaggtgacc cttcgagacc tgtttgaccg cgccgctcgtc ctgtcccaact acatccataa 180
cctctctca gaaatgttca gcgaattcga taaacgggtat acccatggcc gggggttcat 240
taccaaggcc atcaacagct gccacacttc ttcccttgcc accccgaag acaaggagca 300
agcccaacag atgaatcaaa aagactttct gaggctgata gtcagcatat tgcgacctg 360
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgagggc 420
tactctatcc aaagctgtag agattgagga gcaaaccaaa cggttcttag agggcatgga 480
gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tctgaagtg 660
ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgttagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcatgtaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gcttttagtag tgtcagtctg 180
actacattct tgaggcattt cagctactct gtagtggtac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 95

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gaggtcattg agaagccaga gaatcctgaa acanccacaca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaattgtc aacatggccc 120
ttaccacagc ccagccagca caacccacaga tcctcttacc acaatattac tgatgtgtgt 180
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgnctgg gttgcttgcc 360
ccaggg
```

<210> 96

<211> 2723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2723)

<223> prolactin receptor (PRLR) gene.

<400> 96

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gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
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ccttggaatta tgtggaagatt cacaaggtoa acaagatgg tgcattatca ttgctacca 186 0
```

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```

aacagagaga gaacagcggc aagcccaaga agccccggac tcctgagaac aataaggagt 1920
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```

<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

```

gtacagttac cttttattta tagcgaaaat gggttttttc atttacagag taacaaagat 60
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tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttccnt ttgggggggg atagggngac cccctttgca 300
gagagggggt aggtgggggt tccccccggn acacacaggc aaggggtttg gngccccttg 360
tgggg                                           365

```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

```

nattcggcac tagggggcac ctgaccacac gccccacag gctctgacca gcagcctatg 60
agggggtttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggt 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300

```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc ctttttttn aggtttntt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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aactgaccac agttgacatc gtcacctga ggggtgctgt cctgagggg gtgcgatgga 480
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gcccctatct 540
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aaaataagta caat 4034
```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 100

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aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaaactt cttggcatcc ttcattgcctt acagctacct agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctcccct tgccaaagggt ggggccaaac ataatttttg cttttctggc ccttcaaaaa 420
catatttcen tcgcgttttg gggg 444
```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

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<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
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acccttgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctagcaaatac 120
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctogtttaac 180
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
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ccacaccacc cctccagctg ggtcacccgcc ntgggttttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
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acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccct tggaggagag 120
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgctggt 180
acctgccctc tatttattag ccaactgttt cctgctgaa tgcctcgctc ccttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc tttccgcttt tgaaagaagc aagacaagt 360
ggccttggtg aggggcaagg ttagggccca ggagccctn gggaagtttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor-related protein (PGF)
gene.

<400> 103
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tccccgggac ccgcctgccc ctgggcgcc cgccccgcc ggccgctccc cgtcgggttc 120
cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa 180
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240
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ggctcgtcag aggtggaagt ggtacccttc caggaagtgt ggggccgcag ctactgcccg 480
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```

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein
ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

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ttcgtatgga taataatgca gcagctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309
```

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

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gctagccgaa tgaagcagag agctgcaaag catctaatag aacgctacta ccaccagtta 120
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gagatgatcg ctatggaaaa tcctgcagac ttgaagaagc agttgtatgt ggaatttgaa 1680
ggagaacaag gattgatga gggaggtgtt tccaaagaat tttttcagct ggttgtggag 1740
gaaatcttca atccagatat tggatgttc acatacgatg aatctacaaa attgttttgg 1800
tttaatccat cttcttttga aactgagggt cagtttactc tgattggcat agtactgggt 1860
ctggctattt acaataactg tatactggat gtacattttc ccatggttgt ctacaggaag 1920
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agtttaaaag atttatttga gtatgaaggg aatgtggaag atgacatgat gatcactttc 2040
cagatatcac agacagatct ttttggtaac ccaatgatgt atg atctaaa ggaaaatggt 2100
gataaaaatc caattacaaa tgaaaacagg aaggaatttg tcaatcttta ttctgactac 2160
attctcaata aatcagtaga aaaacagttc aaggcttttc ggagaggttt tcatatgggtg 2220
accaatgaat ctcccttaaa gtacttattc agaccagaag aaattgaatt gottatatgt 2280
ggaagccgga atctagat tt ccaagcacta gaagaaacta cagaatatga cggtggctat 2340
accagggaact ctgttctgat tagggagtgc tgggaaatcg ttcattcatt tacagatgaa 2400
cagaaaagac tcttcttgca gtttacaacg ggacagaca gagcacctgt gggaggacta 2460
ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaaggtt acctaca tct 2520
catacttgct ttaatgtgct tttacttccg gaataactca gcaaagaaaa acttaaaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttggca tgctgtaa 2628
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106

```
aattttaatt ctagcacctg aagctataca agggatgtct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagncgg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
ggggnggggt ttcttgaggt aggttatggt ggact gggnc caaggntggg ggggtaccacc 360
cag 363
```

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107

```
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgctgttgtt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatattc ta tgtgggtcaaa tatttggact 180
catttaggac ttagatattt cagtgtactt gatTTTTTaa ttttaactctt tttcacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgTTTTTgtt tgtaataataa aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408
```

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108

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atggccgcgg cggctggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgtaacg 120
gattatgac caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccggtag atattttgga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg cttcctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctacagagtaa aggatcgtga tgagttccca 360
atgatTTTaa ttggtaataa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600
```

gtcattttct ag

6 12

<210> 109
<211> 592
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(592)
<223> 5' terminal sequence. tyrosine kinase with
immunoglobulin and epidermal growth facto r
homology domains (TIE) gene.

<400> 109
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgatgt ctggctcttt ggagtccttc tttgggagat 1 80
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagt ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccattccagcc 480
agaactnggt ctgttgccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592

<210> 110
<211> 3845
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3845)
<223> tyrosine kinase with immunoglobulin and
epidermal growth factor homology domains (TIE)
gene.

<400> 110
cgctcgctcct ggctggcctg ggtcggcctc tggagtatgg tctggcgggt gccccctttc 60
ttgctcccca tcctcttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggctcgga cgctggggc cc gcccctgc tgctggagaa ggacgaccgt 240
atcgtgcgca ccccgcccg gcccacctg cgctggcgc gcaacgggtc gcaccaggtc 300
acgcttcgcg gcttctccaa gccctcggac ctctggggcg tcttctcctg cgtgggcgggt 360
gctggggcgc ggcgcacgcg cgtcatctac gtgcacaaca gccctggagc ccacctgctt 420
ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacaccctg 540
gactggcatg aagcccagga tgggcgggtc ctgctgcagc tcccaaattg gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc ccttgggcag cg ccttcttt 660
cggctcatcg tgcggggttg tgggctggg cgctgggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcactg gcaccgcgtg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

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caggagcagt gccaggcat atcaggctgc cggggcctca cttctgcct cccagacccc 900
tatggctgct cttgtggatc tggctggaga ggaagccagt gccaagaagc ttgtgcccct 960
ggtcattttg gggctgattg ccgactccag tgccagtgtc agaatggtgg cacttgtgac 1020
cggttcagtg gttgtgtctg ccctctggg tggcatggag tgcactgtga gaagtacagc 1080
cggatcccc agatcctcaa catggcctca gaactggagt tcaacttaga gacgatgcc 1140
cggatcaact gtgcagctgc aggaacccc ttcccctgc ggggcagcat agagctacgc 1200
aagccagacg gcactgtgct cctgtocacc aaggccattg tggagccaga gaagaccaca 1260
gctgagttcg aggtgccccg cttggttctt gcggacagtg ggttct ggga gtgccgtgtg 1320
tccacatctg gcggccaaga cagccggcgc ttcaaggtca atgtgaaagt gccccctgtg 1380
cccctggctg cacctcggct cctgaccaag cagagccgcc agcttgtggt ctcccctgtg 1440
gtctcgttct ctggggatgg accatctcc actgtccgcc tgcactaccg gccccaggac 1500
agtaccatgg actggtcgac cattgtggtg gacccagtg agaacgtgac gttaatgaac 1560
ctgaggccaa agacaggata cagtgttcgt gtgcagctga gccggccagg ggaaggagga 1620
gagggggcct gggggcctcc caccctcatg accacagact gtcctgagcc tttgttgacg 1680
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aacttcggcc aggtcatccg gg ccatgatc aagaaggacg ggctgaagat gaacgcagcc 2640
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gaagttctgt gcaaattggg gcatcacccc aacatcatca acctcctggg ggcctgtaag 2760
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ctgcggaaaa gccgggtcct agagactgac ccagctttg ctcgagagca tgggacagcc 2880
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gagaacctag cctccaagat tgcagacttc ggcctt tctc ggggagagga ggtttatgtg 3060
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caaaccccca ctccagctcc ttcgcttaag ccagcactca caccactaac atgccctgtt 3780
cagctactcc cactcccggc ctgtcattca gaaaaaata aatgttctaa taagctccaa 3840
aaaaa 384 5

```

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(202)
<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111
aaagcccttc aaggtttact cncctcactt gcaaggccca cancttggtc aaggaccaa 60
cccacaggct ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
accatgggg canantnatg ag 202

<210> 112
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(450)
<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112
attcaagtac cttttcctac acagcggta gatagcatca gacctgcatt gaacagtcct 60
gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgaggt ggaagtggag 180
cccagtgaag tggaagactt cgaggctcgt gggagcgtt tctccaagtc tgctgatgag 240
agacagcgca tgtgtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgcccg ccttcagaga gctttcctnc ccttcggaaa 360
ggtgccgttc ctttgaacc ccgtgaacc ctgncgttcg aaaggattgc ttggcttgcc 420
cgccgcggga aacggaggct ttcagaagca 450

<210> 113
<211> 1810
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1810)
<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113
ggggggaagg ccaagcagt accaggaaga gggagaaact tctgctcaga ccgagcgtgt 60
gccactggac ctgagtcctc gcctggagga gacgctggac ttcggcgagg tggaagtgga 120
gcccagtgag gtggaagact tcgaggctcg tgggagccgc ttctccaagt ctgctgatga 180
gagacagcgc atgctggtcg cagcgttaagg acgaactcct ccagcaagct cgcaaactgt 240
tcttgaacaa aagttctgaa gatgatgcgg cctcagagag cttcctcccc tcggaagggtg 300
cgtcctctga ccccgtagc ctgcgtcgaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgtcctc tgccttcctc agctgcct cc tgcgcctgt 420
gcccagactga ctggaggagg cctgtcccaa ttctgccgct ccatggaaaa gcggttga 480

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ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
tccttctttg taatactttc tatgtgacat ttctcttccc cttagaaaca ctgcaaattt 600
taactgtagg tatgatctct tctggg gttg actggactgc ttgggggtgg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
gtcccacaaa tgcaggtgtc ctgagcacca caccagtgga gaagagtgtg ggggagggcg 780
acagtgtgag cccgccccca cgtcgtgggg taacatctgt tatcaaactg ctgtcgttgt 840
tgtggaagca tgtagactgt gccagagcca gaccacggg ctcatgcacc cctgagcagc 900
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agtgtgcccc atgggtcccc tcccctctca gcatttcctt gtcccgtctg gacctgggga 1140
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cactgcgttt tcctagctgt gttattcctg gtttaattca gcagagaagg taagggtgtga 1380
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tttaaggatt tgaacatga agtcataggt tacagacctc agttttatgc cccattgga t 1500
tacttttttt tttttttttt tttttttact ctttgaaagc tttgttttgt ggtagtcgct 1560
tttggaaga atccagtatt atctacaatt attggcaaag tttaaatgta ttttacataa 1620
cggaagttt ttagaatgtt gaaaagtaat tgaaaagggt gataggtaaa tttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaat 1740
tctgtgcatt tttttttttt aatttgttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc 1810
```

<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
cdna dkfzp434c136 (from clone dkfzp434c136) (EST
R81127) gene.

<400> 114

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gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtntccn actttttaca tgtgtacaat gtttcacat gtnccaatta atggttgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggg ccaacacaat tttttttttt aatgggnctt 240
gccacctt 248
```

<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 115

```
ttttttaaag cagctttoga aatatcaacc acagcattaa acattgaaca gagtacattc 60
caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt cccaccattt gattttnttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accggggnac ttttttttg tcagggtttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggccgggg 360
ggtcaattat ncctggacac ctcaattcaa ggcntccttt gggggtttgg gggcc 415
```

<210> 116

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 116

```
aattgtgcca gaaaagcatt ttagcaattt atacaatatc atccagtacc ttaagccctg 60
attgtgtata ttcatatatt ttggatacgc accccccaac tccaataact ggctctgtct 120
gagtaagaaa cagaatcctc tggaacttga ggaagtgaac atttcggtga cttccgcatc 180
aggaaggcta gagttaccca gagcatcagg ccgccacaag tgcttgcctt t aggagaccg 240
aagtccgag aacctgcctn tgtcccagct tggaggcctg gtccctggga ctgagccggg 300
gccctcactn gcctcctcca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
tgggnetgtt cacctggggg ccctncaggt agngccntt tttcacgt 468
```

<210> 117

<211> 6030

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6030)

<223> b-cell cll/lymphoma 2 (BCL2) gene.

<400> 117

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taaccgggag atagtgtatg agtacatcca ttataagctg tcgcagaggg gctacgagtg 120
ggatgcggga gatgtgggag ccgcgccccg gggggccggc ccgcgcggg gcatcttctc 180
ctcgcagccc gggcacacgc cccatacagc cgcattcccg gacccg gtcg ccaggacctc 240
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acctgtggtc cacctgaccc tccgccaggc cggcgacgac ttctcccgcc gctaccgccg 360
cgacttcgcc gagatgtcca ggcagctgca cctgacgccc ttcaccgcgc ggggacgctt 420
tgccacggtg gtggaggagc tctt caggga cgggggtgaa tgggggagga ttgtggcctt 480
ctttgagttc ggtgggttca tgtgtgtgga gacggtcaac cgggagatgt cggccctggt 540
ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca cctggatcca 600
ggataacgga ggctgggatg ctttgtgga actgtacggc cccagcatgc ggcctctgtt 660
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tgattttctcc tggctgtctc tgaagactct gctcagtttg gccctgggtg gagcttgcac 720
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 caaaagggtc actaaagcag tagaaataat atgcattgtc agtgatgttc catgaaacaa 840
 agctgcaggc tgtttaagaa aaaataacac acatataaac atca cacaca cagacagaca 900
 cacacacaca caacaattaa cagtcttcag gcaaaacgtc gaatcagcta tttactgcca 960
 aagggaataa tcatttattt tttacattat taagaaaaaa agatttattt atttaagaca 1020
 gtcccatcaa aactcctgtc tttggaaatc cgaccactaa ttgccaagca cgccttcgtg 1080
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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

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<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

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<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 119

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<210> 120
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(319)
<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

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<210> 121
<211> 2372
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

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<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

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<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 123
cgagtgagnt atgttgagg aacatgttgt gtctgccgtt tttgaatacc cagggtggga 60
gcttgccat ctgcatcccc acttoccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggetcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 124
gccagggtc agtgggcaag ggctctgtgc cgtngncctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgagg tgatcgacga 120
aggetgttg cgtggtatg ggccggatca tntgttingca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagtgt acattcagca ctcttcagg gaataggggac 300
ccccagttga ggattgaggc ntcagggttc cctccggnnt gggcagattc agccttttca 360
ccccaaatgg cagcaattgg cntgggtgat ttcccacaaa tcnttctctg cattcccccg 420
acctttccca gacagtttg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain-containing protein
hip-55 (HIP-55) gene.

<400> 125

```
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accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgctggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aagtgatgt acgccttctg cagagtgaag gacccaact ctggactgcc caaatattgtc 240
ctcatcaact ggacaggcga gggcgtgaac gatgtgcga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gccatgtga ccatcaacgc acgggccgag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcttcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttccag gacgtgggac ccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaagg ttggtaaaga cagcttctgg 540
gccaaagcag agaaggagga ggagaaccgt cggctggagg aaaagcggcg gcccgaggag 600
gcacagcggc agctggagca ggagcgccgg gagcgtgagc tgcgtgaggg tgacgcggc 660
gagcagcgt atcaggagca ggggtggcgg gccagcccc agaggacgtg ggagcagcag 720
caagaagtgg ttccaaggaa ccgaaatgag caggagtctg ccgtgcaccc gagggagatt 780
ttcaagcaga aggagagggc catgtccacc acctccatct ccagtcctca gcctggcaag 840
ctgaggagcc ctttctgc a gaagcagctc acccaaccag agaccactt tggcagagag 900
ccagctgctg ccatctcaag gccagggca gatctccctg ctgaggagcc ggcgcccagc 960
actcctccat gtctggtgca ggcagaagag gaggctgtgt atgaggaacc tccagagcag 1020
gagaccttct acgagcagcc cccactggtg cagcagcaag gtgccggctc tgagcacatt 1080
gaccaccaca ttcagggcca ggggtcagc gggcaagggc tctgtgccg tgccctgtac 1140
gactaccagg cagccgacga cacagagatc tcctttgacc ccgagaacct catcacgggc 1200
atcgaggtga tcgacgaagg ctggtggcgt ggctatgggc cggatggcca ttttggcatg 1260
ttccctgcc actacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag ccccaatccc aacccacact ccaggccaat acatgccctc 120
gggactggct cagtcccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tactcttc cagtcaccc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggtgggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcaggcgagg ttttncagg gaggncccg gaggacggc ttgggtnttg g ggtaagggc 360
ttaanccagt cnggctttg gtaagggcc gynaaggat tccntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(339)
<223> 5' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 127
gtggatgagg tgcgcgactg cagaaggcca tggggcgtn gccgctgatt cagggcgagt 60
acatgatccc ctgtgagaag gtgtccacc c tggccgcat cacactgaag ctgggaggca 120
aaggctacaa gctgtcccca gaggactaca cgctcaaggt gtcgcaggcc gggaagaccc 180
tctgcctgag cggcttcatg ggcattgaca tcccgcacc cagcggnac tctggatcct 240
ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggg 300
tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128
<211> 1988
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1988)
<223> cathepsin d (lysosomal aspartyl protease)
(CTSD) gene.

<400> 128
ccatgcagcc ctccagcctt ctgccgctcg cctctgcct gctggctgca cccgcctccg 60
cgctcgtcag gatcccgctg cacaagttca cgtccatccg ccggaccatg tcggagggtg 120
ggggctctgt ggaggacctg attgccaaag gccccgtctc aaagtactcc caggcgggtg 18 0
cagccgtgac cgaggggccc attcccaggg tgctcaagaa ctacatggac gccagttact 240
acggggagat tggcatcggg acgccccccc agtgcttcac agtcgtcttc gacacgggct 300
cctccaacct gtgggtcccc tccatccact gcaaactgct ggacatcgct tgctggatcc 360
accacaagta caacagcgac aagtccagca cctacgttaa gaatggtacc tcgtttgaca 420
tccactatgg ctccggcagc ctctccgggt acctgagcca ggacactgtg tcggtgcctt 480
gccagtcagc gtcgtcagcc tctgccctgg gcggtgtcaa agtggagagg caggtctttg 540
gggaggccac caagcagcca ggcatacct tcacgcagc caagttcgat ggcatacctg 600
gcatggccta cccccgatc tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
agcagaagct ggtggaccag aacatcttct ccttctacct gagcagggac ccagatgcgc 720
agcctggggg tgagctgatg ctgggtggca cagactccaa gtattacaag ggttctctgt 780
cctacctgaa tgtcacccgc aaggcctact ggcagggtcca cctggaccag gtggagggtg 840
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tcattgtggg cccggtggat gaggtgcgcg agctgcagaa ggccatcggg gccgtgccgc 960
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acacacaccc acacactcgc ccgcccactg tcctgggcgc cctggaagcc ggccggccaa 1380
gcccgacttg ctgttttgtt ctgtggtttt cccctcctg ggttcagaaa tgctgcctgc 1440

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ctgtctgtct ctccatctgt ttggtggggg tagagctgat ccagagcaca g atctgtttc 1500
gtgcattgga agaccccacc caagcttggc agccgagctc gtgtatcctg gggctccctt 1560
catctccagg gagtccccctc cccggcccta ccagcgcccg ctggctgagc ccctacccca 1620
caccaggccg tectcccggg ccctcccttg gaaacctgcc ctgcctgagg gcccctctgc 1680
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ggaggtggg ttgggattgg gggctggtgc cagccttcct ctgcagctga cctctgttgt 1920
cctccccttg ggcggctgag agcccagct gacatggaaa tacagttgtt ggctccggc 1980
ctcccctc                                     1988

```

<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 129

```

gtggcggcac tcattgttct cgggtcacgc ccgttccca cagtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atgtccctg gacacaggtc ccacattcc ttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tcctgatggc ccccgagta atgttctca 300
ggttgtaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggtttnttg gaaggagntt ttcca                                     385

```

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 130

```

tttttttttt ttttgagaaa ggaattttca tcccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt ccccgacctc gctgtggggg ctctgttttc tctccgcgc gctctcgtc 120
tggccgacga gtgga gaaat ctgcgggcca ggcacogaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacggtgatc gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctoggagacc ttttcccaa cctcacg gtc 360
atcccgcggt ggaaactctt ctacaactac gccctgtgca tottcgagat gaccaatctc 420
aaggatattg ggctttacaa cctgaggaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactggtccc tgatcctgga tgcggtgtcc 540
aataactaca ttgtggggaa taagcccca aagga atgtg gggacctgtg tccagggacc 600

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atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
 tggaccacaa accgctgcca gaaaatgtgc ccaagcacgt gtgggaagcg ggcgtgcacc 720
 gagaacaatg agtgcgtgcca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
 acggcctgtg tagcttgccg ccactactac tatgcccgtg tctgtgtgcc tgccctgccg 840
 cccaacacct acaggtttga gggctggcgc tgtgtggacc gtgacttctg cgccaacatc 900
 ctacagcgccg agagcagcga ctccgagggg tttgtgatcc acgacggcga gtgcatgcag 960
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 tctctcaga tgcctcaagg atgcaccatc ttcaagggca atttgtcat taacatccga 1140
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 gccacaacca ccagtccag ccgaagcagg aacaccagc cgcagacac ctacaacatc 2340
 accgaccggg aagagctgga gacagagtag cctttcttg agagcagat ggataacaag 2400
 gagagaactg tcatttctaa ccttcggcct ttacattgt accgcatcga tatccacagc 2460
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 acctgctgat ccttgatoc tgaatctgtg caaacagtaa cgtgtgcgca cgcgcagcg 4200
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87/292

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gactgccctt gctgtgtgct tcaaggccac aggcacacag gtctcattg c ttctgactag 4920
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tgaaccggc 4989
```

<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

```
gggcaacaat ctggcagctg agctagaagc caacctcggc ctcatgaag aaatttcagg 60
gtatctaaaa atccgccgat cctacgctct ggtgtcactt tcttcc ttcc ggaagttagc 120
tctgattcga ggagagacct tggaattng gaactactcc ttctatgcct tggacaacca 180
gaacctaaag cagctctggg actggagcaa acacaacctc accatcactc aggggaaact 240
cttcttccac tataacccca aactctgctt gtcagaaatc cacaagatgg gaaggaaagt 300
tcagggaacc aaggggncgc cagg aggaga aacgacattt nccctggaag gaccaatggg 360
gggaccaggg catcctgttg aaaaatggag tttactttta anttttgctt taacattngg 420
gacntttttt tggacaagtt ttttggtgaa gttggggagc cctnattttg 470
```

<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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ccagcgccgc gcgctgatc cgaggagacc ccgcgtccc gcagc catgg gcaccggggg 120
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cctcacggtc atccggggat cagcactgtt ctttaactac gcgctgggtca ttttcgagat 480
 gggtcacctc aaggaaactcg gcctctacaa cctgatgaac atcacccggg gttctgtccg 540
 catcgagaag aacaatgagc tctgttactt ggccactatc gactgggtccc gtatcctgga 600
 ttccgtggag gataatcaca tcgtgttgaa caaagatgac aacgaggagt gtggagacat 660
 ctgtccgggt accgcgaagg gcaagaccaa ctgccccgcc accgtcatca acgggcagtt 720
 tgtcgaacga tgttggaact atagtcaactg ccagaaagt tgc ccgacca tctgtaagtc 780
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89/292

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<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

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<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

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<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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 aaaaattccc tcgctatcaa ggaattaaga gaagcaacat ctccgaaagc caacaaggaa 2460
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```

agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
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tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
cacacacaca taaaaaatgt tccttttgct tttaaagtaa tttttgactc ccagatcagt 5460
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atattcattt cc 5532

```

<210> 138

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 138

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ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtgc aaagtgtgcc 60
tacagtatac aaggtaaact cacaactcat caaaactaaa actttttaca atgtgcaata 120
catgtaggga tattaattca atatataaat gtcacatgtc tcccaaagt caccaggct 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttatc ctaaaacttat gtatacttct ctaaagattc ttagggttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggnc cgagtg 378

```

<210> 139

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 139

```

gctttcactg gcatgggaga cccttgacac ctgtgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtagatccca 120
tgcattgatac tatgtagtat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaaat cagaatgcct gtttgtggtt tcatatgcaa taatatattt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgtccta 300
ggatattttg atatttacct ttatgttgga atgctattaa atgttttccn gtgtccaaag 360
taaaatattg ttttaaaaac ctaacaatgg accccgatag tacag ggtta agtgagggga 420
accttatgga ttctaacaag tcctagg 447

```

<210> 140

<211> 4138
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4138)
<223> tek tyrosine kinase, endothelial (venous
malformations, multiple cutaneous and mucosal)
(TEK) gene.

<400> 140
cttctgtgct gttccttctt gcctctaact tgtaaacaag acgtactagg acgatgctaa 60
tggaagtc caaaccgctg ggtttttgaa aggatccttg ggacctcatg cac atttgtg 120
gaaactggat ggagagattt ggggaagcat ggactcttta gccagcttag ttctctgtgg 180
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gctggaagt actcaagatg tgaccagaga atgggctaaa aaagtgtgtt ggaagagaga 420
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caggatacga accatgaaga tgcgtcaaca agcttcttcc ctaccagcta ctttaactat 540
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agatgcagtg atttcaaaa atggttctct catccattca gtgccccggc atgaagtacc 660
tgatattcta gaagtacacc tgcctcatgc tcagcccgag gatgctggag tgtactcggc 720
caggtatata ggaggaaacc tcttcacctc ggcttccacc aggctgatag t cgggagatg 780
tgaagcccag aagtggggac ctgaatgcaa ccatctctgt actgcttgta tgaacaatgg 840
tgtctgcat gaagatactg gagaatgcat ttgcccctc gggtttatgg gaaggacgtg 900
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aaacgtgatt gacactggac ataactttgc tgtcatcaac atcagctctg agccttactt 1560
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agaatatgaa ctctgtgtgc aactggtccg tcgtggagag ggtggggaag ggcatcctgg 1740
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```

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```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

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taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaacttta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcagggttt acatggggac 300
attattgaac attttcgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggttc angacatgtt cacia 395

```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

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tcgtaattgg catcaacttc atggaaagaa agaagcgat gacacattga ttaaagatct 60
caaaaaagcc aatctttgta ctcttgag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgc tcagaaaatt caaacttcag aaatgaaatc caaagcttg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgt tgaaaagatt cttaatagct 240
ggctgtaaat actgcttggt tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccaacatat ttgtagggtt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagtggg ggaacaaac ttccttcaag ggttaaatgc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

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gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccc ggcgagctg cctcttctcc cgcggttg tggaccgct cagtacggag 180
ttggggaagc tcttctactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgctc aaaagtgtta atgcccaagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttggaa ggctgcac atgatggcca attctgcat aagccctgtc ctccagggtga 420
aaggaaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaga 480
aggggaaggag tacacagaca aagcccatth ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggcttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
cagatgtaaa ccaactttt ttgttaactc tactgtatgt gaacactgtg accctgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcacaaga 720
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aattataatg ttgactatt atatatgtgt atgcatttta ctggctcaa actacctact 1920
tctttctcag gcatcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
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tccatttttg ccttggtgct catcttaat g gcctaattgca cccccaaca tggaaatata 2040
accaaaaaat acttaatatg ccacaaaag gcaagactgc ccttagaaat tctagcctgg 2100
tttgagagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
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ggaaccacct aaagaacttc catttatgga ggattttttt gccccttggtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

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aaagtcacta agaatcattt attnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tgagagaaac ggaaccagga cacatgggga gccgagagaa aacagtccag gccagtatgt 180
tacaggagct ggaaggtnnt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcaac gttagtcca ggaagacaa ctactcccag ccccatatga 300
gccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttcgct ggctaattca aagtgaatg aactggggag ggatgggggtg gatgaggaag 420
gttcgntgga cggt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgtgc ntncagggg a gcaggctgaa ggggtccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcggcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgccac aggaagcctg cagtccctga agcgcgaggg 180
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ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

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gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttgcgcgagg caccgaggca 60
ctcagaggag gcgcatgtgc agaaccggct ggggatgtcc gtcagaacct atgcgcgagc 120
aaggcctgcc gccgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttgccttgg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaag accatgtgga cctgtcactg 420
tcttgtaccc ttgtgcctcg ctcaggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgcccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tcctcatgta cataccttgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta acaaaaaact aggcggttga atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcatcccggtg 840
ttctcctttt cctctctccc ggaggttggg tgggcgggct tcatgccagc tacttccctc 900
tccccacttg tccgctgggt ggtacctctc ggaggggtgt ggtccttcc catcgctgtc 960
acaggcgggt atgaatttca ccccttttcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaaggg gcctcaccga gtgggggcat catcaaaaac 1080
tttgagtgcc cctcacctcc tctaagggtg gcaggggtga ccctgaagtg agcacagcct 1140
agggttgagc tggggacctg gtacctcctt ggctcttgat accccctctt gtcttgtgaa 1200
ggcaggggga aggtggggta ctggagcaga ccaccccgcc tgcctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc ccctgtacct 1320
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tgtccctccc ccttgtcttt cccttcagta ccctctcatg ctccagggtg ctctgagggtg 1440
cctgtcccac cccaccccc agctcaatgg actg gaaggg gaaggagacac acaagaagaa 1500
gggcacccta gttctacctc aggcagctca agcagcgacc gccccctct ctagctgttg 1560
gggtgagggt cccatgtggt ggacagggcc cccttgagtg gggttatctc tgtgttaggg 1620
gtatatgatg gggagtaga tctttctagg agggagacac tggcccctca aatcgtccag 1680
cgaccttctt catccacccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcag acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
ctgaagtgct tagtgtactt ggagtattgg ggtctgacct caaacacc tt ccagctcctg 1920
taacatactg gcctggactg ttttctctcg gctccccatg tgtcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtctttc 2040
acagctcttc ccacaatgct gaataacag caggtgtctc ataatgatt cttagtgtgact 2100
ttaaaaaaaa aaaaaaaaaa a                                     2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac cccccggagt acagcttctt tggtaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcatcttg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaaact tggtaggggt agggaggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gtcacctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tcccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtcttc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggg gaatttcac agaatgatca agttgacgac aggaaggaa gcgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgagc aggatcccc aaggatgcaa 300
cggattcgct gctgtg tca tcatgactgt ttgctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgct ac 120
ccaagaactc ttaccatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

```
cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagttta gcaactcggg gacgagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgtgcc 480
acctgttttg ctagaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgctga gtccctctt ccttggaac ctccacca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc ctggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata ccaaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaagga attc 854
```

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

<221> misc_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150

```
ggttgagcac aggnacttt attgatgna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttctcttnt gctcttntg 180
gggntggtgg nccagggn tn ttactccttg gaggccatnt gggc 224
```

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151

```
gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatc tctctgccc ctctgctgat gccccatgt 120
tcgtcatggg tgtgaaccaa gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcacccctgg gccaagggtca tccatgacaa ctttggatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359
```

<210> 152

<211> 1283

<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttcg acagtcagcc gcattcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtccgagtcac acggatttgg tcgtattggg 120
cgccctggta ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catgggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgcc ccatgttctg catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaacttgg gtatcgtgga agga ctcatg 600
accacagtcc atgccatcac tgccacccag aagactgtgg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagtgaac ggggaagtca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggg gaagcaggcg tcggaggggc ccctcaaggg catcctgggc 900
tacactgagc accaggtggg ctctcttgac ttcaacagcg acaccactc ctccacctt 960
gacgctgggg ctggcattgc cctcaacgac cactttgtca agctcattc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgggt gacctcatg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagtgtg 1200
ccatgtagac cccttgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcggtgttga gta ccaggcg gcggggccag 180
ctccntant ncgccccctc ttccccctcc tgttaaatac acaaataat tatattcaat 240
ntgaatcng tcnttttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcggang ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t                                     361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto-oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaaggtga agacgctcaa ggccgagaac 120
gcgggngtgt cgagtaccgc cgcttctctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagc aa cggctntnag ctgctgcttn gggcaaggg acacgccttc 240
tggaacgttc cctgccccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttcccactn ggggtccagg gtacgaggcg gtgggnacc cacctggggg acntaggggg 360
cgnccgcaaa ccacattngg atttccggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto-oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggtc tttgcgcaca gctgccggtc ggctgctacc 120
cgcccgcgcc agcccccgag aacgcgcgac caggcaccca gtccgggtcac cgcagcggag 180
agctcgcgcg tcgctgcagc gagggccgga gcggccccgc agggaccctc cccagaccgc 240
ctggggccgcc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcggtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420
cggaccccgc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgcgtct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgtgata acgacgacgc ctacaccccc gggacagtac ttttaccctc gcgggggtgg 600
cagcgttgga ggtgcagggg gcgcaggggg cggcgctacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgctaccg gggggccccc ggctgggccc gggggcgtct acgccggccc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgcgggg gctgcgctcg ggaccgggag ctcgtaaccg acgaccacca tcagctacct 900
cccacacgcg ccgcccctcg ccggtggcca cccggcgag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagccggg acgccacgcc 1020
gccggtgttc cccatcaaca tgaagacca agagcgcatc aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgccca ccaagtgcgg gaagcggaag ctggagcgca t cgcgcgct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgcggcct 1200
cctccgggag caggtggccc agctcaaaca gaaggtcatg acccacgtca gcaacggctg 1260
tcagctgctg cttggggtca agggacacgc cttctgaacg tcccctgcc ctttacggac 1320
acccctcgc ttggacggct ggacac acgc ctcccactgg ggtccaggga gcaggcgggtg 1380
ggcaccacc ctgggacctt ggggcgcgcg aaaccacact ggactccggc cccctaccc 1440

104/292

tgcgcccagt ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500
tttttttctg ctggaacacag actcgattca tattgaatat aatataattg tgtatttaac 1560
agggagggga agagggggcg atcgggcg agctggcccc gccgcctggt actcaagccc 1620
gcggggacat tgggaagggg acccccgcct cctgcctcc cctctctgca ccgtactgtg 1680
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60
ggtagaagct agagggccag tctttctgctc tcaggccctc aagtcctctt tagagagacc 120
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaacccgg 180
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
ggtcaaagaa agcaagaccc tgcaagaggc atcccagtga cccccagaag tgactggggg 300
aaggggagcg ctatcctagg anggtggggg tgggt 335

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 157

gcctggactt gtcttgggtt ccagaacctg acgaccggc gacgcgacgt ctct ttgac 60
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120
accatgccca acttctcttg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaaacctc caccaccgtg 300
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
gcagaagttc ctgaaggng aggggccccca agacntcttg gacngagaa tttccccacg 480
t 481

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgagg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120
cctcccgcg cgcaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaag 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaagggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aaggagagg gccccaagac ctggtggacc agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accaggggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgccttg cttcactgcc ccct ccgtcc caccctctcc ttctaggata gcgctcccct 660
taccacagtc acttctgggg gtcactggga tgcctcttgc agggctctgc tttctttgac 720
ctcttctctc ctcccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tccgggttca ctcccgcct cccaagtca gcagtctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa                                     969
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcgntgga ggggaggtgg ccccgntcc gccgangaan tcgccccg cc acccgagag 60
cncncagagg gaccattgac cttgggtcc ccaggaaaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga ccctgtgaag ccgtctcggg gcccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tgggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggagntct tgcagggggg gcgccccacc gatttcgttc aacc                                     344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccac acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccaggga ggggagccct gagccactcc 180
ctgtgggtgg cagtcaactgt ccaggagggt cccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaacacgggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcgagccc ctcccgggt ccagcccgggt ccggggccgc gccggacc c agcccggcgt 180
ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggctagcgc cccgccacce gcagagcggg cccagaggga ccatgacctt gggctcccc 300
aggaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctggtgac ctgcaag tgt gagagcccac attgcaagg gcctacctgc 420
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caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgacctt gggccccgtg 660
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cagaccccca ccatccctaa ccggttggt gcagaccgg tccctctcagg cctagctcag 1680
atgatcgagg agtgctggt cccaaacccc tctgcccagc tcaccgcgct gcggatcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatgggtgcc 1860
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162

gtgacctgac gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgcccctcac catctcacgg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180
cacagaaccg catcaagggc tgccacgac acctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gccagtgcc cctgatgaca gcaagggtca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnnggcagan caagnct ggg gtttttncat atggaca 407

<210> 163

<211> 1130

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1130)

<223> lim domain protein (RIL) gene.

<400> 163

tgagagtccg gctcaggctc cggctgcggc tccagcccgc gatgcccacat tccgtgaccc 60
tgcgcgggcc ttccgcctgg ggcttcggcc tgggtgggccc ggacttcagc gcgcccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
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tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
ccagcgctga cccagcagag gcctcccggc gagccgggag cagagtcgac ctgggctccg 600
aggtgtacag gatgctgcgg gagccggccg agcccggtggc cgcggagccc aagcagtcag 660
gctccttcgg ctacttgtag ggcattgtag aggcggcgca gggcggggat tggcccgggc 720
ctggcgggcc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgcaggggct gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
aacgggacaa gctctaccat cccgagtgtc tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccagggc tacgacgtgg tggcggtgta ccccaatgcc aaggtggaac 1020
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccgggtg 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctgtc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

anattcgga cgagggatcc ctctatgtc aacgtccaga acctagacaa ggcccggcaa 60
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agccttcga agatgctctt cgctgc etc cacctcccca gtcggtgtcc 180
atgntcagc agctccgagg ggagccctgg gttccatggg aagctgagcc ggcgggaggc 240
tgaggcactg ctggcagctt caatggggat ttcnggtac gggagagcac gaccacacng 300
gggcaatatg 310

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain -containing) transforming protein 1 (SHC1) gene.

<400> 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat 120
accccttgc tggccccctt gccaaaactg gcaggggggc caggctgggc agcagccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
ccccatcagc ttcattccctg ggccccatcc tgctcctct gctggggac gatagtcca 360
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ggcgccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
gggcagccat gccagagtca ggccccctac cctcctcca ggacatgaac aagctgagtg 540
gaggcgggcg gcgcaggact cgggtggaag ggggccagct tggggcgag gagtggaccc 600
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca 660
tgggaccggg ggttctctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720
tgctgtccct ggacttcaac acccgactc aggtcaccag ggaggccatc agtctggtgt 780
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
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ttgccaggga tgcatcagc accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140

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```

tcaggaaccc acccaaactg gtcacccctc atgacaggat ggctggcctt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
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cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
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agcc

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3664

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

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```
gagcacaggg tntttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggtcttac tccttgaggg ccatgtgggc atgagggtcca ccacctgtt 240
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagcnttc gaagggtggg gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccagga tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde -3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```
tggtcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggctg gagtcaacgg atttgggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tgttgccatc aatgaccctt tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttccagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttaaccac ctttgagaa gggtttggg gttcatttn 420
caaggggggg gagcccaaan ggtcttcat tttttggccc cttttt 467
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<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

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ggcttggtgt tntntctct ttttgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggcgc ccctcccacc agcctgagac cgctctctgc ctctctcctc 120
tcctctcttc tccagcatct cac ccacttt ctctcttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tctgtagcc cctgctttct aagtcaccc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagtntccac aggggctagt 300
ccctgggnt acctgc 316
```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

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atctcccat ccagacctac tctgcctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggctcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac cctgtctc actgtccct gaagccagcc ttcttccatc 240
ccaggagcac cacacca gc ctctcgtcct ccccttcaca gctctggac cctcctcac 300
tgggccattc cctcgtggtt cccaacagc ggacataggc ccatccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aaccacagtt gttgaggctt tgggtgtttg 420
ggcagttgag ttgaggcttt                                     440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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gcctcgcgc cgccgtcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcgcac cttcggcggc gcccgggct tcccgcctcg ctcccgcgtg agctcgcgcg 180
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ccgacgcggg gaaccaggag ttctgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtcg ctctcctggag cagcagaacg 480
cgctcgcgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggagg gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tggatgcagc tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
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atggggagggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcca ccagagaccg tcctcaccct tgtcctcact gctccctgaa gcccagcctt 1560
```

112/292

```

cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgaccctcc 1620
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gtctcttact ttctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
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tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
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```

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

```

gatccacgcc cgctacatcc ttaccaacgg tggcatcgcc agatgttga aaagtaccag 60
caaggagact ttggttactg tccctcgtgtg tactgtgaga accagccaat gcttcccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccga gtgcatggat 180
gtgtacacac ccaagtcac cagacacat caccagcatg ggccgctac t ttccgactg 240
gtttccctca catgctcttc atgggtgcat cccaggtacc ggcccagggt gaccttgcca 300
accagtttgt gccagggtt ttacggtttt caaggttcca tncgggtggg cttaccagg 360
tgcaggt 367

```

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

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tgccgggggt atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact ccgtgtcccg gcattccacg cggcacctga ccttggcgc ttgcgtgttg 180
ccctctccc caccctccct aatttccact cccccaccc cacttcgct gccgcggtg 240
ggtccgcggc ctgcgtgta gcgg tcgccc ccgttccctg gaagtagcaa cttccctacc 300
ccacccaggt cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggagg 360
gtcctggatt tccgtgttct gtgggtccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaattttac tggactcaat gagcaggtcc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

```

113/292

```

ccagagtgac ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgccta 600
catccttacc aaccgtggca tcgcccagat gttggaaaag taccagcaag gagactttgg 660
ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc ttccagacat 720
cccagtgtaa gccatggtga agctctactg cccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctacatgct 840
cttcatgggt catcccgagt accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
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ttttcctttc ttttttgcca ccctttcagg aacctgtat ggtttttagt ttaaattaaa 1080
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<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

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gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
cggaagttct gttggnatga gagagacttg tctacaggca ggnaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgctgca cggtagaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggttnagtgg ggaatctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn ggggtcaagggt gggctctacc 360
ccgtccnttg agctctngtg tncactncgc ttgggggatc cctccca cttcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475

```

<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```

ggtcatctct tgcctgaagc tgagatatgc tgaccagcgc ctgtcttcag actgtgaaga 60
ccagatccga atcattatcc aggagtcgcg cctggactac cgcctggatc ctgagctcca 120
gctgcactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgacccggg 300
acttcatact tgcttggtgc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat gggaaggcac tgggagggtt aaggcgggtt 420
gaggtttaca gcccagattg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483

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<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
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ccagggcgtc ccacagccag ggccagggtc ccggggccaa ctttgtgtcc ttcgtagggc 180
aggccggagg cggcgggccg gcgggtcagc agctgcccc gctgcctcag tcatcgagc 240
ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccc cagccgcctt 300
tcccggcggg tgggcctccg cggcggggag gagcgggggc tgggggggc tggaag ctgg 360
cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420
acaacctggc ggtgctcgag tgctgcagg atgtgaggga gcctgaaaat gaaatttctt 480
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600
aaccggttgg aaaaggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
agtatcagtg tcaccagtac attaccaaga tgacggccat cttttttagt gattaccgtt 720
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gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900
aagccattct ccgggtggct gagctgtcat cggatgactt tcaacttaga cggcatttat 960
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ctgggtcaga ttaccgcatt gatcgagctt tgaatgaagc ttgtgaatct gtaatccaga 1560
cagcctgcaa acatataaga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620
tatacacaga gaagatggta gaagactgtg aacaccgtct ct tagagctg cagtatttca 1680
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gttccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580
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cagagctaga ctacaccctc atgagggtct gcaagcagat gataaagagg ttctgtccgg 2700

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taaaccatcat gtttagaaaa gcctgtaaag ctgacattcc taaattctgt cacggatatcc 2880
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tgccctttgtt tggcaaacct gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
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aaaccacca 3909
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<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

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attaaaatct tcttctttca ctatcgtagc ttaaaactctg tttggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaaat 360
gggtttctag gcatatgtat tatggctatt 390
```

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gccccctgg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgcccctg 300
 tcgcggatct ggggagagga gagaggctt ccgcctgaca gggccactcc gcttttgcaa 360
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 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
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 ctgctggcag aggactggcc atttggagct gagatgtgta agctgggtgcc tttcatacag 780
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgctc tgagtattga cagatatcga 840
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 tatatttaatt ttctatttaa atttttagatt atttttatta ccatgtactg aatttttaca 3540
 tcttgatacc ctttcttct ccattgtcagt atcatgttct ctaattatct tgccaaattt 3600
 tgaaactaca caca aaagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

117/292

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aaggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
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<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

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acancagaga tccatttatt acagtcctgc aaccccgact gccacccct tgggaattct 60
tgccctctgc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnttcat tgttctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
gggggcccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
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taaccccgag ccaggccaaa ttgaaaagt gctgggntt tt 462
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<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

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agcagctcca accagggcag ctttctgag aagatgcaac caatcctgct tctgctggcc 60
ttctctctgc tgcccagggc agatgcagg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
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ataaatgtca ctttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gaccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360
```


118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca aggccaggt gaagccaggg cagacatgca gtgtggccg ctgggggcag 480
acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540
gatcgaaagt gcgaatctga cttacgcat tattacgaca gtaccattga gttgtgcgtg 600
ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660
aacaagggtg cccaggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
tgcaccaaag tctcaagctt tgtactctgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
tacctggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900
agtccagatt tactctggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2;
pfeiffer syndrome) (FGFR1) gene.

<400> 180

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aaaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
tttttcttt ttgttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
caggggcan caacactgcc cccaacctgg gccttcgect caccatectc tgggtaccgg 360
gcntttgggt caggcaaaag aaactagtnt cgggtttatt angccactgg naccacctt 420
ttgggggcag aggtcacctt cattcgaggg caclangcac tgacctcctt t 471

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

gctttgtgc cagccacttc atcccctccc agatgttga ccaacacccc tccctgccac 60
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ttgctttgct gaccaaagtc ctgggtacca gaggatggg aggcgaaggc aggttggggg 360
cagtgtgtg gccnggggccc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

cctcttgccg ccacaggcgc ggcgtcctcg gggcgggcg gcagctagcg ggagccggga 60
cgccggtgca gccgcagcgc gcggaggaac cggggtgtgc cgggagctgg gcggccacgt 120
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cgcaggggcga tggagccggt ctgcaaggaa agtgaggcgc cgccgctgcg ttctggagga 360
ggggggcaca aggtctggag accccgggtg gcggacggga gccctcccc cgccccgcct 420
ccgggggcacc agctccgggt ccattgttcc cgcccggtc ggaggcgccg agcaccgagc 480
gccgcgggga gtcgagcgcc ggccgcggag ctcttgcgac ccgcgcagga ccggaacaga 540
gcccgggggc ggccggccgg agccggggac gcgggcacac gccgcctcgc acaagccacg 600
gcggactctc ccgaggcgga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660
gagctcactg tggagtatcc atggagatgt ggagcctgt caccaacctc taactgcaga 720
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gtcatcgtgg agtatgcctc caagggcaac ctgcgggagt acctgcaggc ccggaggccc 2460
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120/292

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gacctggtgt cctgcgccta ccaggtggcc cgaggcatgg agtatctggc ctccaagaag 2580
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tgctatatat taaaaacaaa aaagaaaaaa aaggaaaatg tttttaaaaa ggtcatatat 4020
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<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

```

cagttatata cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagggtgtaac cagctcctcg aggagatata 120
ccccaaccac cagggtcatc tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgacg aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccacatg gttagcagaa gatctgcccc tccaccaagg cagtgaaggg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaacttgt gtgnatctgt cnggtcttct ggtttccctg gagga 415

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<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

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tactgcggtg agagccagcg ggccagcgcc agcctcaaca gcgcagagaa gtacacgagg 120
aaccggcggc ggcgtgtgcg ttagggcccg tgtgcgggcg gcggcgcggg aggagcgagg 180
agcggcagcc ggctggggcg ggtggcatca tggacgagaa ggtgttcacc aa ggagctgg 240
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cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgtttagaa 420
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ccaatggcct cacgttggtg tctagagctc accagctagt gatggaggga tataactggt 960
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agacttaatt gtaaaaccaa ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatggt ttcaggtaga g                                     2181
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<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185

cgaagaggat gaggaagagc tnetgctgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg gcggnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagcccgaa gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
ggggttaaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gttcctgagg 360
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186

gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
gaggaggggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcagggtg 180
gggcacttct ccttctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
ccctgatggg tgacttcgca ggcgtagact ttgtgtttct cgtagtctgc ttgtgctcagc 300
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ctgggggant taccnattt gggagggcgt tatccacctt ccaactgtact ttggc ctctc 420
tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acattncitt tgatccncca 540
ct 542

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MC1R) gene.

<400> 187

atcacctgca gtcctatgct gtccagcctc tgcttctggt ggcctatcgc gtggaccgct 60
acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcggaag 120
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180
gaccacgtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
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<210> 188

123/292

<211> 1270
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1270)
<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MC1R) gene.

<400> 188
ggagaggggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catggggggac 60
acccaaggcc ccttggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggccctccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
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ctgctggtga gcgggagcaa cgtgctggag acggccgtca tcctcctgct ggaggccggt 480
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agtgttgaaag 1270

<210> 189
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(336)
<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189
ccaanaccaa atccgagccc ttggacaaa ctgcctgcg ccgagagccg tccgcgtaga 60
gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120
aagaaggagc gaggtcgcnc aagaagccgg ntccgcgggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
tctcaacaat atgtcactg gaga tgacgt ttttagatac gtattgattc accagctgga 60
cattctcggg gggtnngtta g gatggtag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagact ctctcttgt acagctcctn cgctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
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caggacggtg ataactctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180
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gccgagagcc gtccgcgtag agcgctccgt ctccggcgag atgtccgagc gcaaagaagg 480
cagaggcaaa ggggaaggga agaagaagga gcgaggctcc ggcaagaa gc cggagtccgc 540
ggcgggcagc cagagcccag ccttgcctcc ccaattgaaa gagatgaaaa gccaggaatc 600
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attcaagtgg ttcaagaatg ggaatgaatt gaatcgaata aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggctgattc 780
tgagaggtat atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840
caccatcgtg gaatcaaacg agatcatcac tggatgccca gcctcaactg aaggagcata 900
tgtgtcttca gactctccca ttagaatatc agtatccaca gaaggagcaa atacttcttc 960
atctacatct acatccacca ctgggacaag ccattcttga aatgtgagg agaaggagaa 1020
aactttctgt gtgaatggag gggagtgtt catgggtgaaa gacctttcaa acccctcgag 1080
atacttgtgc aagtgcctaa atgagtttac tgggtgatgc tgccaaaact acgtaatggc 1140
cagcttctac aaggcgagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200
catcgccctc cttgtggctg gcacatgtg tgggtggcc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gacccctcgg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

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tcaatcgtat tctaaaaa cg tcatctccag tgagcatatt gttgagagag aagcagagac 1440
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tcttagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
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aaccctgat tctaccgag actctcctca tagtgaaagg tatgtgtcag ccatgaccac 1740
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ggaaatgtct ccaccctgtt ccagcatgac g gtgtccaag ccttccatgg cggtcagccc 1860
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gtttgacat caccctcagc agttcagctc cttccaccac aaccccgcc atgacagtaa 1980
cagcctccct gctagccctt tgaggatagt ggaggatgag gagtatgaaa cgaccaaga 2040
gtacgagcca gcccaagagc ctgttaagaa actcgccaat agccggcggg ccaaaagaac 2100
caagcccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctccagag 2160
cagtaactca gagagtgaag cagaagatga aagagtaggt gaagatacgc ctttctggg 2220
catacagaac ccctggcag ccagtcttga ggcaacacct gcctt ccgcc tggctgacag 2280
caggactaac ccagcaggcc gctctcgcac acaggaagaa atccaggcca ggctgtctag 2340
tgtaattgct aaccaagacc ctattgctgt ataaaaccta aataaacaca tagattcacc 2400
tgtaaaactt tattttatat aataaagtat tccaccttaa attaaacaat ttattttatt 2460
ttagcagttc tgcaataaaa aaaaaaaaaa 2490

```

<210> 192

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. ciliary neurotrophic factor receptor (CNTFR) gene.

<400> 192

```

cagatgctac gccgggaagg agtacattat ccagggtggca gccaaaggaca atnagattgg 60
gacatggagt gactggagcg taccgcccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tgcggagacc acgaccagca ccaccagctc cctggcacc 180
ccacctacca cgaagatctg tgaccctggg gagctgggca gcggcggggg accctcggca 240
cccttcttgg tcagcgtccc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagcccg gcaccccatg aggacatgca gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtagaccccg gtttctattt t ncacacggg caggaggant 420
ttttgcattn tttttnagac acaatttttt gga 453

```

<210> 193

<211> 1566

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1566)

<223> ciliary neurotrophic factor receptor (CNTFR) gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgccggcg gaggctcgcc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgctcgct gccggggcg gtcggaaggc 120
gcggcgccgaa gcccgggtgg cccgagggcg cgaactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccctg aagagtttgt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctctgtccc gtgggcctgc tgtgtgtgc 300
ttgccgcgc cgccgcagtt gtctacgcc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtga aatgggacag acctggcccc tgacctgctc aacggctctc 480
agctggtgct ccattggcctg gaactgggcc acagtggcct ctacgcctgc ttccaccgtg 540
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tctgtgagaa ggaccagcc ctcaagaacc gctgccacat tgcctacatg cacctgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
ctatcacctt tgacgagttc accattgtga agcctgatcc tccagaaaat gtggtagccc 900
ggccagtgcc cagcaaccct cgccggctgg aggtgacgtg gcagacccc tcgacctggc 960
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agcctgcaga ccccggtttc tatttt gcac acgggcagga ggacctttt cattctcttc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac acactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccgctcccc atcatcgta tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtgtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttctgtgctg 240
gtctgggtct gacccaccg acctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgccaaa ccacagggcc ngggatgaca gatactgtg 349

```

<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(729)

<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195

```
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ttgggtctac cacacctcct tttgccctcc gcaggagcct gtgttggaag agatggtgat 120
gggcctgggc gttttgttgt tggctcttgt gctg ggtctg ggtotgacct caccgaccct 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggccgggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aaacctcaca gagaaaacct aagaataagc aagtcttctt tccaggtcac 420
cacttgcaag ctacatggag gttcccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgtgttgt cttgtgaaaa tggcttaoct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccctg gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttcccc tctgcacca gaacagtgtt ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg ttttctgttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt                                     729
```

<210> 196

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196

```
ngttactcca gccttggacc ggggctgcca ctt ggagagn cgtggcgacc acaaggagggc 60
gcacatcctg agggctcctg cgggccactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgccaccg gggatctcga tgccgtcctc atcctgcagg gtcccccta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgctggg ccagcattgt cttnatattc ttgccttcca gcttgcggtt gttagggttg 420
cagaccttaa ccgcnaccgt ttccagacca tt                                     452
```

<210> 197

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

```

aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcatg 60
aagacagtcc tatggcttcc tggctttgag acccggtctt gggacgcagg gctaccgtgc 120
agctgagggg gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360
ccggcttcga tgggtgtttt                                     379

```

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

```

cctgggcccgg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgctgct gtcactgcca tccattggag ccagcaccc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccgcgtccct gtgtccactt 180
ctcctgaccc ctcggccgcc accccagaag gctggagcag ggacgccgtc gctccggccg 240
cctgctcccc togggtcccc gtgcgagccc acgcccggccc cggtgccgc ccgcagccct 300
gccactggac acaggataag gccacgcga caggccccc cgtggacagc atggaccgcg 360
gcacgctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtggggccc cgagagggg c gaggtgacat 480
ataccactag ccaggctctc aagggtcgcg tggctcaggc cccaatgcc atccttgaag 540
tccatgtcct ctccctggag ttcccaacgg gcccgctcaca gctggagctg actctccagg 600
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gtgtcttcct gcattctccag gccctgg gaa tcccaactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttccccaaga 780
cccagatcct tgagtgggca gctgagaggg gccccatcac ctctgctgct gagctgaatg 840
acccccagag catcctctc cgactgggcc aagcccaggg gtcactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcacgc tgcagtggcg gccgcgtact ccagccttgg 960
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gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tgggtgccttc ctcatcgggg 2160
ccctgctcac tgctgcactc tggtagatct actgcacac gcgtgag tac ccaggcccc 2220

```

129/292

```
cacagtgagc atgcccgggcc cctccatcca cccgggggag cccagtgaag cctctgagg 2280
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ccccagcaa gcgggagccc gtggtggcgg tggctgcccc ggcctcctcg gagagcagca 2400
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cccaggagac agaccacttg ccacgctgtt gtaaaaaccc aagtccctgt catttgaacc 2760
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tgaaacctga aaaaaaaaaa aa 3142
```

<210> 199

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(402)

<223> 3' terminal sequence. epidermal growth
factor (beta-urogastrone) (EGF) gene.

<400> 199

```
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acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402
```

<210> 200

<211> 4877

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4877)

<223> epidermal growth factor (beta-urogastrone)
(EGF) gene.

<400> 200

```
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agctggaact ttccatcagt tcttccttct ttttctctct ctaagccttt gccttgctct 120
gtcacagtga agtcagccag agcagggtctg taaactctg tgaaatttgt cataagggtg 180
tcagggtattt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240
```

ccttggcagg ctgcattcag aaggtctctc agttgaagaa agagcttggg ggacaacagc 300
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 ggtcaatcat actcaccttg cccggggccat gctccagcaa aatcaagctg ttttcttttg 420
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 gtcgagcaga gatgtgagga gtcgcaggcc tgctgacact gaggatggga tgtcctcttg 3720
 ccctcaacct tggtttgttg ttataaaaga acaccaagac ctcaagaatg ggggtcaacc 3780
 agtggctggt gaggatggc aggcagcaga tgggtcaatg caaccaactt catggaggca 3840
 ggagccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

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```
taagggtcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gacccttgaa gggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaaaac tggattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttctttc aaaagtagag 4140
caaaactata ggttttggtt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtcttatttc 4260
caagtaagag tactgggaga atcactaggt aacttattag aaacccaaat tgggacaaca 4320
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tcctgcagcc ccagaagaaa ttaggggtta aagcagacag tcacactggt ttggtcagtt 4440
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tattacaata ccgttaagat acagtgtagg catttaactc ctcattggcg tgggtccatgc 4560
tgatgatttt gccaaaatga gttgtgatga atcaatgaaa aatgtaattt agaaactgat 4620
ttcttcagaa ttagatggcc ttatttttta aaatatttga atgaaaacat tttattttta 4680
aaatattaca caggaggcct tcggagtctc ttagtcatca ctgtcctttt cccctacaga 4740
attttccctc ttggtgtgat tgcacagaat ttgtatgtat tttcagttac aagattgtaa 4800
gtaaattgcc tgatttgttt tcattataga caacgatgaa tttcttctaa ttatttaaa 4860
aaaatcacca aaaacat 4877
```

<210> 201
<211> 153
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(153)
<223> 3' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

```
<400> 201
attagacctc acattaggga aaacatcaaa atgantcacg cagcaccctt gagatcctga 60
ggttggtcca gccgagcccg tgctcagaag cccccagct cgggccccca gctgcccga 120
cgcccgccct caccagcagg cagggtccca tcc 153
```

<210> 202
<211> 472
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(472)
<223> 5' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

```
<400> 202
agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgctg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttata ctgagacaaa ccactgcaga ttggtggtg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggaacc atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaaactcg 300
```

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aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatccntc agtctctnt tgttgacat tttgcgtggc nt 472

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hnrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

cactgcgctt gcgcgggttg agggcggttg ctacgtctcc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcgagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcaggagaa gagcctgctg agtgcagtga ggccgggtctc 240
ctgcaggagg gagtacagcc agaggagttt gtggccatcg cggactacgc tgcaccgat 300
gagaccacgc tcagtttttt gagaggagaa aaaattotta tcctgagaca aaccactgca 360
gattggtggt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcatect ggacgtgggc 600
tgtgggactg ggatcatcag tctcttctgt gcacactatg cgcggcctag agcgggtgtac 660
gcggtggagg ccagtgaagt ggcacagcac acggggcagc tggctcctgca gaacggcttt 720
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aggacgcacg catatcagcc cgtgtaccct gtgacagtga ctgtccccc ctcctgtgtt 1860
agtgtgccc ttactgccgt cgtcatcca ctctgtggg acgtaggatt gcaca gggct 1920
gtgccagtgg cgtgtaggga aactgccct ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgacatg ctcaataaat attttaaat agtgaaaaaa aaa 2093

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt  tatta aggtc  tggcagatgt  ggtggagggtg  gaagtacaaa  cccaggcctg  60
ggcctaggaa  agggcagaag  aaaggcaaag  ggtcccttgg  agcaggaacc  catccctctc  120
tgcttatacc  cagcaccctt  catcccaggt  tcctttcttc  aacctccgcc  tgctcttggg  180
aacacagagc  accaagaact  gacaaaccgg  gaccctccag  gggccacagc  gtgggggc  ag  240
agtccagggn  ttctgtctcc  ccgcagtggg  gagatctngg  ggagctcagg  tgaacctcct  300
cancctcctg  ccagtatgaa  gttggggaag  cgccttttct  tgtccccag  aacagaacaa  360
actcttggtc  tctgtgggtt  ngggggaaaa  ggtttnnggg  ggtttggact  taggggagaa  420
gttnagcttg  a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtcccctgcc  cctgcccttg  gacagtgcgc  cctacagncc  tttccccggg  cagagaacgg  60
aatttcctga  gatcctctgg  cacctcccag  ccccaccctg  gccatgggta  cctcggggaa  120
catagctccg  tcttcagca  gccctggga  catttgccac  tccttcacat  ctcagggagg  180
gggcccggaa  cccctcccag  gcccctacc  aacaccagct  gtggagccc  tgcccacct  240
atccccagca  gagctttaag  caagaatacc  atgatcccct  gtatggaaca  gggngggggc  300
agccaggccg  tgggaaccag  ggtgggggt  tcaatggggg  cacagggtac  ccaggggggn  360
ggggggttg  ttgattcaaa  acagggaaca  gacgggattt  tt  ggnttaag  gatttnaggt  420
tntttaancg  gggtg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

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```

agaccccagt cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
caggggactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacia 240
acgtggacat gtactcgcc cagagagatg cccagggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcncggac 420
attntagaa gagcatctgc ccggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin a11 (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggtccc ccagtgcgcc gagtgccccg cgggccccgc gagcgggagt 60
gggaccagc cctaggcaga acccaggcgc cgcgcgccgg acgccccgg agagagccac 120
tcccgccac gtccatttc gccctcgcg tccggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgccccagg tggctacca ccagctgcac caggtggtgg 240
tccctgggga ggtgctgcct accctcctcc gccagcatg ccccccacg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
gtctgggaca tttggaggag ccaac atgcc caacctgtac cctggggccc ctggggctgg 420
ctaccacca gtgccccctg gcggttttgg gcagcccccc totgccagc agcctgttc 480
tccctatggg atgtatccac ccccaggagg aaaccacccc tccaggatgc cctcatatcc 540
gccataccca ggggccccctg tgccgggcca gcccatgcca cccccggac agcagcccc 600
agggggcctac cctgggcagc caccagtgc ctacctggt cagcctccag tgccactccc 660
tgggcagcag cagccagtgc cgagctaccc aggatacccg gggctctggga ctgtcacc 720
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gtaccacgac atctcgggag atacttcagg ggattaccgg aagattctgc tgaagatctg 1680
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tcaccgtcct agagcttagg cctgtcttcc acccctcctg accggtatag tgtgccacag 1860
gacctgggtc ggtctagaac tctctcagga tgccctttct accccatccc tcacagcctc 1920
ttgtctgctaa aatagatggt tcatttttct gaaaaaaa 1958

```

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttcccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tatcctgggg caaaaggggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgaggtt ttic gttcga agacagaatt 360
ggacagttga ggacagttat tgtctttntt taaaagnaca aggaaggttt cagnttgggt 420
tacccecaag gag                                     433
```

<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

```
ggccccctcag ccctgctgcc cagcacgagc ctgtgctgcg cctgccccaac gcagacagcc 60
agaccaggg cgccccctct ggcggtctctg ctccctccga aggatgcttg gggagtgagg 120
cgaagctggg cgctcctctc ccctacagca gcccccttcc tccatccctc tgttctcctg 180
agccttcagg agcctgcacc agtctgcct gtcccttctac tcagctgtta cccactctgg 240
gaccagcagt ctttctgata actgggagag ggcagtaagg aggacttcct ggagggggtg 3 00
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ggcttcggg tgcatgccg gctctggccc tcaaaggcga gctgctgttg ctgtctctcc 420
tgttacttct ggaaccacag atctctcagg gcttggtcgt cacacccccg gggccagagc 480
ttgtcctcaa tgtctccagc accttggttc tgacctgctc gggttcagct ccgtggtgt 540
gggaacggat gtcccaggag cccccacagg aaatggccaa ggcccaggat ggcaccttct 600
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acaatgactc ccgtggactg gagaccgatg agcggaaacg gctctacatc tttgtgccag 720
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```

tgggcacact acaatttggct gagctgcac ggagccggac actgcaggtg gtgttcgagg 1380
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 cttgacttag agtgacagcc ggtgtcctgg aaagccccc gcagctgcc cagggacatg 4920
 ggaagaccac gggacctctt tcaactacca cgatgacctc cgggggtatc ctgggcaaaa 4980

137/292

```

gggacaaaga gggcaaatga gatcacctcc tgcagccac cactccagca cctgtgccga 5040
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ttacaaatat ttttaggact cacgttaact cacatttata ca gcagaaat gctattttgt 5520
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```

<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSCR14) gene.

<400> 210

```

gaccggcgta tcacacacat ctccgaggac aggaagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcatgggct cgtgagcaca ctcaagtccc agcccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttcgagg aggaggccca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccggcac aggggtaccc attcacacac cagcgttttg 300
accagatgcg agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
gttctggggg ntctcagcat cctnattccg gcctctgttt tgagtc 406

```

<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSCR14) gene.

<400> 211

```

ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgcccagccc agactcggac 120
tcggacacag actcggagga cccgagtctc cggcgagc g cgggcggctt gctcgcctcg 180
caggatcatcc acagcgggtca cttcatgtgt tcgtcgccgc acagcgactc gctgccccgg 240
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aagtggaaga atttcaa agg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggta tatccagtat gtgaagcggg ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
ctggagggga actactggaa gcggcgcatc gaggtgtgta tgcgggaata ccacaagtg g 600

```

138/292

```

cgcatctact acaagaagcg gtcocgtaag cccagcaggg aagatgacct cctggcccct 660
aagcaggcgg aaggcaggtg gccgcgcgcg gagcaatggt gcaaacagct cttctccagt 720
gtggtccccg tgctgctggg ggacccagag gaggagccgg gtgggcggca gctcctggac 780
ctcaattgct ttttgtccga catctcagac actctct tca ccatgactca gtccggccct 840
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cccgtgggtg actcctctt cagcagtggg accctgggcc cagaggtgcc cccggcttcc 1080
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agcagggcag gcatcatg tg tgtgtgtgtg tgtggatgtg tgtgtgtggg ttttgtaaag 3240
aattcttgac caataaaagc aaaaactgtc tgctggttaa aaaaaaaaaa aaa 3293

```

<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility
complex, class ii antigen-associated) (CD74) gene.

139/292

<400> 212

```
cctttggcct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cttttctgcc 120
gacccttagt tccctctgct cagccaagct tgttatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa                                     207
```

<210> 213

<211> 1304

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1304)

<223> cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 213

```
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tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctgggccc ggcgccctgg 120
ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcctgggtgac 180
tctgtctctc gctggccagg ccaccaccgc ct acttcctg taccagcagc agggccggct 240
ggacaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgag catggccacc ccgtctgtga tgcaggcgct 360
gcccatggga gccctgcccc agggggcccat gcagaatgcc accaagtatg gcaacatgac 420
agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtgt acccgccact 480
gaaggggagc ttcccggaga acctgagaca ccttaagaac accatggaga ccatagactg 540
gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcactcctt 600
ggagcaaaag ccactgacg ctccaccgaa agagtcactg gaactggagg ac cgtcttcc 660
tggtctgggt gtgaccaagc aggatctggg ccagtcctcc atgtgagagc agcagaggcg 720
gtcttcaaca tcctgccagc ccacacagc tacagctttc ttgtctcctt cagccccag 780
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tcacccttgt acaagacaaa ccaagtggga acagcagata acaatgcagc aaggccctgc 900
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ggaccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag                                     1304
```

<210> 214

<211> 355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(355)

<223> 5' terminal sequence. annexin a7 (ANXA7) gene.

140/292

<400> 214

```

aggaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttgga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctccatggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatccn ggccctcttc 240
atgcctccta cgtattacga tgcctngagc tttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatttt ngtgcacang atcanattca ggtaa 355

```

<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

```

gaacccggtc tcccgcaaga tggagccggg ttgggctgtg acgctgctgc tggggtcaga 60
atgtcatacc caggctatcc cccaacaggc taccacacct tccctggata tcctcctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatccct atccatagtg ctttcctcca 180
atgggaggag gtgctaccc acaagtgcga agtagtggt acccaggagc tggaggctac 240
octgcgccgt gaggttatcc agccctgga ggcctatcct gtgccccaca gccaggggga 300
gtccatcct atcccgaggt tctccaggc caaggatttg gaggccacc agg tggagca 360
ggcttttctg ggtatccaca gccacattca cagtcttatg gaggtgttcc agcacagggt 420
ccactactcg gtggctttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttaccta gtcagatcaa tacagattct ttttcttcc atcctgtttt ctctcctgtt 540
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ccagctgcc aactcgatgc tataagagat gcagaaattc ttcgtaaggc aatgaagggt 660
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caaaaaatta aagcagcatt taagacctcc tatggcaagg atttaataca agatctcaaa 780
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ataaaaaatt gcatat 2176

```

<210> 216
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(525)
<223> 3' terminal sequence. thrombospondin 1
(THBS1) gene.

<400> 216
tcctgnanta nctncaacaa ccgatgtgag ggaaaatcgg tccagacacg gacctgccac 60
attcaggagt gtgacaagag atttaaacag gatgggtggc ggagcntgng ttccccgtgg 120
tcatcttgtt ctgtgacatg tggatggtgt gtgatcacia ggatccggct ctgcaactct 180
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tctttttaat tgaaaaacaa attcaccntt ttccccagct ttttttcctt gtgttcaggg 480
gaggcagagg ttttttgaac gggnttaggg gatttttgc aagtt 525

<210> 217
<211> 5722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5722)
<223> thrombospondin 1 (THBS1) gene.

<400> 217
ggacgcacag gcattccccg cgcccccca gccctcgccg ccctcgc cac cgctcccgcc 60
cgccgcgctc cggtaacacac aggatccctg ctgggcacca acagctccac catggggctg 120
gcctggggag taggcgtcct gttcctgatg catgtgtgtg gcaccaaccg cattccagag 180
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ctgctggccc tggagcggaa agaccactct ggccaggctc tcagcgtggt gtccaatggc 480
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gactatgaca agacatgtgt gggagaccgc ttgacaact gtccctacaa ccacaacca 2460
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cagctggaact ctgac tcaga ccgcattgga gatacctgtg acaacaatca ggatattgat 2700
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<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catttcatac actcattaaa aacacttaac 120
acatccaatt aaaggttctg caaagtcttc tgctggtggg tgctcttcat cccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta ggcgagcctc 240
actttagttt cgggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggctgc aggaatattc tcaaggctat ggaatattag ggngtctggt ncaat cttgg 360
ggcccttttt tcttttttctg ttncattttct ccattta 397

<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180
gatcaactga gattctcata catggctata atagaaggag caaatgtat aaagggagat 240

tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220
<211> 2287
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2287)
<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220
ggggggcctg agcctctccg ccggcgcagg ctctgctcgc gccagctcgc tcccgcagcc 60
atgccaccca ccacgcagcg ggaattcgaa gagttggata ctcagcgtcg ctggcagccg 120
ctgtacttgg aaattcgaaa tgagtcccat gactatcctc atagagtggc caagtttcca 180
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240
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gtttggcagc agaagaccaa agcagttgtc atgctgaacc gcattgtgga gaaagaatcg 420
gttaaatgtg cacagtactg gccaacag at gaccaagaga tgctgtttaa agaaacagga 480
ttcagtgtga agctcttgtc agaagatgtg aagtcgtatt atacagtaca tctactacaa 540
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tgaaaaatct gttactaaaa aaaaaaattg tatgtcgatt gaattgtact ggatacattt 1920
tccatttttc taaaaagaag tttgatatga gcagttagaa gttggaataa g caatttcta 1980
ctatatattg catttctttt atgttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
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tcaggtaaac agttgtgcaa gactttgtaa agaaattggg ttctgtaaat cccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280
taaaccc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgta tcttcattga gctcaagttt 180
actgtacgtg actgcaacag cttccctggg tggcgccant tcttggcaag gagactttca 240
acctctacta tgccgagtcg gacctgggac tacggcanca acttncagaa ggcgcct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
cggaagtgc gcgcaggccg gcgggcggga gcggacaccg aggccggcgt gcaggcgtgc 60
gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcattggagc 120
tccaggcagc ccgcgcctgc ttcgccctgc tgtggggctg tgcgctggcc gcggccgcgg 180
cggcgcaagg caaggaagtg gtactgtctg actttgtctg agctggaggg gagctcggct 240
ggctcacaca cccgtatggc aaagggtggg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggctccgca 360
ccaactgggt gtaccgagga gaggctgagc gtaacaactt tgagctcaac tttactgtac 420
gtgactgcaa cagcttcctt ggtggcgcca gctcctgcaa ggagactttc aacctctact 480
atgccgagtc ggacctggac tacgg cacca acttcagaa gcgcctgttc accaagattg 540
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atgtgcgccg caccgagggt ttctccgtga ccct ggacga cctggcccca gacaccacct 1620

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agttgcagat gattcaaac g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of
 metalloproteinase 1 (erythroid potentiating
 activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

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ggaacagggt ggacactgtg caggcttcag cttccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctccc aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttggg ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagcaa 240

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cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccacctgca gttttccagc aatnagaaac 360
tcctcgttng cggtttttgg ggacnnttgg aagtntc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc 437

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

gccncagatc cagcgccag agagacacca gagaaccac catggcccc tttgnagccc 60
ctggcttctg gcacctctgt g ttgctgtgg ctgatagccc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggcttctgc aattccgacc tcgtcatcag ggccaagtgc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagttt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagtttng 420
tgggttcctt gggaacagtc tgaggtttag ttnagcggtn ggggtt 466

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

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ccatggcccc ctttgagccc ctggcttctg gcacctctgt gttgctgtgg ctgatagccc 120
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggcttctgc aattccgacc 180
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acaaccgcag cgaggagttt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420
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agggttcca gtcccgtcac cttgcctgcc tgccctggga gccagggctg tgcacctggc 6 60
agtccctgcg gtcccagata gcctgaatcc tgcccgaggt ggaactgaag cctgcacagt 720
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gc

782

<210> 226
<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(353)
<223> 5' terminal sequence. ephrin -a1 (EFNA1)
gene.

<400> 226
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
tgaaggtagc tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120
agaagagact tgcagcagat gaccagagg tgccgggttct acatagcatc ggtcacagtg 180
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aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
caggcactcc aaacctgtct tgggggccac ttccagagcc ccagccctt ggg 353

<210> 227
<211> 1480
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1480)
<223> ephrin-a1 (EFNA1) gene.

<400> 227
gcggagaaag ccagtgggaa ccagaccca taggagacc gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccaacacg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtga accggcccag 360
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtagc tgtcagtggc aaaatcactc acagtcctca 540
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
ccttccactt ctgctgctgc aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840
gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
aagggggccac gtggatgggc aaagcctgtc aaagatgccc cctccag gag agagccagga 1080
tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggtagt gcattctctc ccattcctgg gcagcactcc 1260

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```
ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagtg tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480
```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> {1}..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```
ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttaactg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatctct gctagtaaac cacagttact taccagtcca taaataaaat 170
```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> {1}..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```
gaattcgcgg ccgcctcttg cggctcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcctgggtc gacgattgtg gagaggcggg ggagaggctt 180
catccatccc acccggtcgt cgccggggat tgggggtccc ggcacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcgcgcg 300
cggagcccgg gacaccggcc accctccgcg ccacccaccc tcgctttctc cggcttcctc 360
tgcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgctt 480
caagatgga accctttgcc tcagggcac cttttggct g gcaactgggtg gatgtgtaat 540
cagtgataat cctgagagat acagcacaaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttcctggg taccactcat caaccacta atttggtcct 660
accagcaat ggctcaatgc acaactattg cccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcac gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgtgat 840
agccagtctt gcccttggag acqttatcta tgtggtcatt gatctcccta tcaatgtatt 900
taagctgctt gctgggcgct ggccctttga tcacaatgac tttggcgat ttctttgca a 960
gctgttcccc tttttgcaga agtcctcggt ggggatacacc gtectcaacc tctgcgctct 1020
tagtggtgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttggttaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tggtaacctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtcfaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260
```



```

cttcgggttc tatttctgta tgcccttggg gtgcactggc atcttctaca cctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggcaac 1560
catgaattca tgtataaacc ccatagctct gtattttgtg agcaagaa at ttaaaaattg 1620
tttccagtc tgcctctgct gctgctgtta ccagtccaaa agtctgatga cctcgggtccc 1680
catgaacgga acaagcatcc agtgggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcactcctcg gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cgggaatctc ttctctgac 1860
cttcttctt aattcactcc cacaccaag aagaatgct ttccaaaacc gcaaggtaga 1920
ctggtttat caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgcgtgt tgaattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
aaatgaaacc agaaggatat ttactacttt tgcatgaaaa tagagctttc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatgtt caatgggaac tggtcacat gaaactttag 2160
agattaacga caagattttc tacttttttt aagtgtttt ttgtccttca gccaaacaca 2220
atatgggtc aggtcacttt tatttgaaat gtcatt tggg gccagtattt tttaactgca 2280
taatagccta acatgattat ttgaacttat ttacacatag ttgaaaaaa aaaagacaaa 2340
aatagtatc aggtgagcaa ttagattagt attttccacg tcaactattta tttttttaa 2400
acacaattc taaagctaca acaaaacta caggccctta aagcacagtc tgatgacaca 2460
tttggcagtt taatagatgt tactcaaaga attttttaag aactgtattt tttttttaa 2520
atgggtgttt attacaaggg acctgaaca tgttttgtat gttaaattca aaagtaatgc 2580
ttcaatcaga tagttctttt tcacaagttc aatactgttt ttcatgtaaa ttttgtatga 2640
aaaatcaatg tcaagtacca aaatgttaat gtatgtgtca tttaactctg cctgagactt 2700
tcagtgcact gtatatagaa gtctaaaca cacctaagag aaaaagatcg aatttttcag 2760
atgattcggg aattttcatt caggtatttg taatagtac atatatatgt atatacatat 2820
cacctcttat tctcttaatt tttgttaaaa gttaactgg cagtaagtct ttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttcaact cttgggggtt 3000
tcagtatgaa cctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
ggcccaagc gacttttgcg gggcattttc ccagatgttt acagactgtg agtacagcag 312 0
aaaatctttt actagtgtgt gtgtgtatat atataaaca ttgtaaattt ctttttagccc 3180
atttttctag actgtctctg tggaatatat ttgtgtgtg gatatatgca tgtgtgtgat 3240
ggtatgtatg gatttaatct aatctaataa ttgtgccccg cagttgtgcc aaagtgcata 3300
gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
agaggcagcg tgaaagcaga tgagctgtgg actagcaata taggggtttg tttgggttgt 3480
tggtttgata aagcagtatt tggggtcata ttgtttctcg tgctggagca aaagtcatta 3540
cacttgaag taattatatt ttcttatcct caattcaatg tggatgaa attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgctg ataataaatt aggtgaagata 3660
atgtgtggg ccataattta ggacaggtaa aataacatca ggttcagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gtccacacca tttgttttag 3840
acaattgtct tttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg cccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

```

<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

```
ggtttcttgt tttttattat tggcgctcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc cctoccacc ccctaaagt ccaaccaag tgagaggggc acagggtgac 240
```

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

```
cttaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggcccttc ttatccgaga gagtgaagc gctcctggg acttctccct ctctgtcaag 180
tttgaaaacg atgtgcagca ctcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tggttggtga agttcaattc ttga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttcca ggggcctttt ttgattttt gattccccag gggggnttgg ngaggttggg 420
ttttccgccg ggggagattt tattccatgt tcntgggtn aatttaggaa ccntt 475
```

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2
(GRB2) gene.

<400> 232

```
gccagtgaat tcgggggct c agccctctc cctcccttcc ccctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gtttcaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40
atgaaaccac atccgtggtt ttttgcaaaa atccccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttctctg ggtgtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatattcc tgccgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattgata actcagacc caactggtgg 660
```

```

aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgatgaac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tgggttggaac tttagggggg gggagggggc 900
gttgatttta aaaatgccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tcactgctgc tcctctttcc cctcctttgt cttttttttc atcctttttt ctcttctgtc 1020
catcagtgca tgacgtttaa ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaaa aaaaaaaaaa ccgaattca 1109

```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```

cgcgcgctct ggctgccnng ntgtacaccg cgccggaaag tggggctcog agggggcgca 60
ctcaaaaccc tgcctttcct ttactttttac tttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctattttat tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tgggttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctgatctcgc cccccccctt cggttctttc gaccgggtcc cccctccctt 300
ttttgtttct gttttgtttt gttttgctac gagtccacat tcctgtttgt aatccttggg 360
ttcgncgggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttcca 446

```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```

ccgaggctat aagaggggcg acaagtggcg cgcgcgagga gccgcccga gtggaggggc 60
ggcgctgctg gccgcccgcg gggcgggcg agggccgagc ggacgggggg gcgcccggcc 120
cccgggaggg cgcgccact cccccccggg ccggcgcgcg gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggctggggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc cccggggcg ccccgacggc cggggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagtg agcaggtggc ggcagcgtc 360
aagcctgcgc ccgcccgcgc ctctacccc cctgcccgcg acggcgcccc cagcgcgcca 420
cccccgagcg gctgctcgc ctctcccgac ctggggctgc tgaagctggc ctccccgag 480
ctcagagccc tcatcatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gaggaggagt tcgcccaggg cttcgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgcgcccgc 660
gccgcccgcg ccggggggcg ctcgggcacg gccacgggct ccgcccccc cgcgagctg 720

```

153/292

```

gccccggcgg cggccgcgcc cgaagcgcc gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtgcgcttcg ctgcggaacc tgtgcccttc 840
ccgcgcgcgc caccgccagg cgcg tgggg ccgcgcgcgc tggctgcgct caaggacgag 900
ccacagacgg tgcccgaagt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
atggacacgc aggagcgcat caaggcggag cgcaagcggc tgcgcaaccg catcgccgcc 1020
tccaagtgcc gcaagcgcaa gctggagcgc atctgcgcgc tgggaagagaa agtgaagacc 1080
ctcaagagtc agaacacgga gctggcgctc acggcgagcc tgctgcgcga gcagggtggc 1140
cagctcaagc agaaagtcc cagccacgtc aacagcggct gccagctgct gcccagcac 1200
caggctccgg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcggggg 1260
ggtgtcgtgg gcgccccgga cttggagagg gtgcggccct ccaccccccc ctccccgagt 1320
gtgcccagga actcagagag gcgcggcccc ggggattccc ccccgaggtg cccaggactc 1380
ggaagggcg ccccgactc gacaagctgg acccctgct cccggggcg agcgcatgac 1440
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gcgtctcggc tgccccttg tacaccgcgc cgcaagggg ctccgaggg gcgcacgtca 1560
aaccctgcct ttcctttact tttactttt tttttcttt ggaagagaga agaacagagt 1620
gttcgattct gccctattta tgttctact cggggaacaa acgttggtg tgtgtgtgtg 1680
tgtttcttg tgttggttt ttaaagaaat gggaagaaga aaaaaaatt ctcc gccct 1740
ttcctcgatc tcgctcccc ttcggtctt cgaccgtccc cccctccct tttttgttc 1800
tgttttgttt tgttttgta cgagtccaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgttt cagtaaagtc tcgttacgcc a 1891

```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```

accaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaatatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
ccggaaccc gaaacggaag ccccgtttaa tgaggaggga tgagctgcc tcctggntca 240
ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggagggggtc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg cntcgaaga cggcatttng gaggaattng aagaggaata c ggttaagaa 420
g 421

```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```
tggaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccaggttg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggtcgcc taggctccgg tacttatgat tacgaatcct ttcccttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc ttcccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cacctatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggagggcg 420
gcctcttctc ttcttagg                                438
```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

```
aaaaattttc tgttaccaaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatggg ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatattat cagtaaatgt aaaatatttg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgtoctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccagggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tcccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcaccagg gcatggggcc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccc gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cacctcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcaccttcca gtectgtcca gctgcatcag 840
cttcgagctc agatttttagc ttataaaatg ctggcccgag gccagc ccct ccccgaaacg 900
ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
cagccgcccg aaccacagac gcagcaacaa cagcagccgg cccttggtta ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gccggtgccc 1140
gcccggggcg gccggccctc gcccgcgccc cccgcagccg cgcagccgcc cgcggccgca 1200
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aaagacaggc gtttagctta ctttttgcag cagaccgatg agtatgtagc caatctgacc 1920
```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
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cctcaaatgat tcagattgaa acaacaaaa agctttt 5257

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

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tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgaggagcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cgnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaga attactgcca aacacaattc tggcctagga aagcgggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tcctcatcag tgggtgtgact 120
ttcttccctt ccttgcatgt cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggcggggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttggttggg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cacgccggcc 360
cttgccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncaggntca agtnccnttt ggtnttnccc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttcct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnnganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcaggggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcagggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctactgctg gggacatcta cctcttatcc 180
accttccgcc tgcccccaa gcagggtgggt gtctcttttg g cctctattc togccaagac 240
aacactcgat ggctggaggg ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaagt ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactcoga ggtccctcca gacctagccc tgccctacat 420
ctctacgtgg actgcaaact ggggtgacca catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggctttg tggaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
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cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
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gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
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cagctgcca atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctggtccga taactgccgc 2040
```


158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgctcgcc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtctaac cagggcatgg aaatcgttca gaccatgaac 2280
agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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gtggcggatt ctggggtgat cattgacaca tccatgcgag gggggcgtct tgggtgtattc 2760
tgcttctccc aagaaaacat aatttggtcc aatctccagt atcgatcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 242

```

cacttttatt tnccttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aacctggac aggacccgca agncaaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctggttt cnggttacag gtttcaggcg cattttnttt tcggaggggg tnttccggt 480
tcgtgagggt aggctgaggg tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 243

```

gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcggttg ctccatcctg gctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc cctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

159/292

ctgggaaatt gcacacacct catgctagcc tcacgaaact ggggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

gtctcagtcg ccgctgccag ctctcgcaact ctgttcttcc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgcgctggt cattgacaat ggctccggca 120
tgtgcaaagc tggttttgct ggggacgacg ctccccgagc cgtgtttcc t tccatcgtcg 180
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acgaggccca gagcaagcgt ggcacacctga ccctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac cttctacaac gagctgcgcg 360
tgcccccgga ggagcaccca gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaacac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgcctctg ggcgcaccac tggcattgtc atggactctg 540
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cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattaggc cccagcaaca cgtcattgtg taaggaaaaa taaaagtgt g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgccgccgg gcagctgtgc ttgctctacc tgtggcgagg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gcccgcgagg agnaagcgtt tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360
gccaaaggtt agggggcaag gtcgtgacat gtgttnacc tattgaaaa aggagcgtt 420
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg tcttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcggtgag 120
cacatgtcac gaccttgccc cctggacett ggctctggac ggtgaccccc atccactgat 180
cttccttgct ttctgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcattggc 240
cccgggcggt ggaatgcga gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300
aagcgtttct gcccgcgagg cccccacgga gcaacagccg cttgtcctcg ggctgcagtt 360
gccagtcat gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag tttgaagggt tgcgcaaggc cgt 473

<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (IT GA6) gene.

<400> 247
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<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

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acaatcaatc catcatntgg ggcacagggt ggttttcggg ggetatttnt tggctttggc 360
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<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2102)

<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

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```

<210> 250

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250

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 ctctt 365

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 251

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<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
gene.

<400> 252

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165/292

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2056

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<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

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<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

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acgggggtga gctgttcttc cactgtccc gggagc gtgt ctccacagag gagcggggccc 960
ggttttatgg tgcagagatt gtctcggtc ttgagtactt gcactcgcgg gacgtggtat 1020
accgcgacat caagctggaa aacctcatgc tggacaaaga tggccacatc aagatcactg 1080
actttggcct ctgcaaaagag ggcacagtg acggggccac catgaaaacc ttctgtgga 1140
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ggtgggggct ggggtgtgtc atgtacgaga tgatgtgagg ccgcctgcc ttctacaacc 1260
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tcagccccga ggccaagtcc ctgcttgcct ggctgcttaa gaaggacccc aagcagaggc 1380
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aggtcgacac aaggtacttc gatgatgaat ttaccgccc gtccatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggacccac ttccccagt 1620
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ctgccatcac cgctgggtgg ttttttacc ctgcc 1715
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<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

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gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagcttcc cattttctta gaggaaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatgggta ctactgcctg ccacgagttc ttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacgggt catggcaaga naggcaggac aggcaagggg 360
tttgagggt tagttaggga gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaagggttg a 431
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<210> 256

167/292

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
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caatattctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggagggt tgtggacaaa 240
gtcatggaaa cactggacaa tgatggagac ggcgaatgtg acttccagga attcatggcc 300
tttgttgcca tggttactac tgccctgccac gagttctttg aacatgagtg agattagaaa 360
gcagccaaac ctttcctgta acagagacgg tcatgcaaga aagcagacag caagggcctt 420
cagcctagta ggagctgagc tttccagccg tgtttagctt aattagga ag ctigatttgc 480
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tggtcttcggc ctgcttcccg ggatgcgcct gatcaccagg tgaacgctca gcgctggcag 900
cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacctatg cgattcaagt cgcggctgca ggatccttgc ctccaacgtg 1020
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gcgttcaata aaaag 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp-binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagtttaaac tatgatttct 60
ctocacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagt tttgctttta 180
actttgaataaatgtcatat ctaaacaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgccttcc 300
tgtgccagca gctgctgatg cgtgccatgc tcttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtagcaaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggtc tcttgacaaa ccttttcacc tactgtatcc agagctgacg 480
tggtctatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgcg 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
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gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaagaa gcagaggccg ctgttcgttt cctttaggtc ttccactaa 360
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cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtgttt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtcaaacatc actaatagaa gtgatataa 720
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aaatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640
aagaattgat gatcctgaaa caaacgcaga gaatagtaac ttgttttcac tattgtttct 2700

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actcttagca attgtaccca tcattgcaat agcaggagtt gttgaaatga aaatgttgtc 3060
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ccagctcctg gagcggttct acgaccctt ggcagggaaa gtgctgcttg atggcaaaga 37 20
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gctggcacag aaaggcatct atttttcaat ggtcagtgct caggctggaa caaagcgcca 4260
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cagtcaagtt cagagtcttc agagacttgc taattaaagg aacagagtga gagacatcat 4440
caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggtgact gtaactgact 4560
gccttgctaa aagattatag aagta gcaaa aagtattgaa atgtttgcat aaagtgtcta 4620
taataaaact aaactttcat gtg 4643

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<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

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caacctttat agtgttatgt caaatagggtc tgacataagc ttaaataaat atatacttta 60
aaaattataa aatatatttaa gttataattht aaaattctca ataaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
aacaatttca agaaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
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atcacatctc tgttttgact gttgggcttt ggttgggttc cagtgggttc gccaggaaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttont cacantccct cagggtnggg ggcgggttng ggnattacc ggcgggggggt 480
tttttc 486

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<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
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tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctcaagtgtc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaagga ttttttcttc caagcaaagg 180
tgaagagacc aagactctga aatctcagaa ttcttttctt aactctccct tgctcg ctgt 240
aaaatcttgg cacagaaaca caatattttg tggctttctt tcttttgccc ttcacagtgt 300
ttcgacagct gattacacag ttctgtcat aaggaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacagggtg ttggatgccc 420
acaggcaaat gcatgggggg gttgtttaat gggg gcaaat ccctacttga atgctctt 478

<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ggtcttacaa cacctccacg gaa gctatga cttatgatga ggccagtgtt tattgtcagc 240
aaaggtacac acacctgggt gcaattcaaa acaaagaaga gattgagtac cttaaactcca 300
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tctgggtagg aaccagaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420
ccaacaatag gcaaaaagat gaggactgag tggagatcta catcaagaga gaaaaagatg 480
tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
cctgtaccaaa tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600
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<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcggt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaataa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatctt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

```

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```

ggagtccgag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tncgcacctc cgacgagcag acgcaggcct tcacgatgac tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
caaganattt cttttgactt tggccccaac ggnagtcttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc cttcaagct tgtnttcgna 300
gaaacccaaa ctggggggct ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gccccgacca cnacaatttc agt                                383

```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```

ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct ccggcctcgt 60
cgtgaagaca cagcgcatct ccccgctgta ggcttctccc acagaaccgg ttctgggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacccatgt gctgggccgt 180
ggaggtcaag aggccccggg gcgtctccct caccaatcat cacttctacg atgag tccaa 240
gcctttcacc tgcctggacg gttcggccac catcccattt gatcagggtca acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagccct gtatatcccc tccaaccggg tcaacgatgg 420
tgttttgtgac tgctgcgatg gaacagacga gta caacagc ggcgtcatct gtgagaacac 480
ctgcaaagag aaggggcgtg aggagagaga gtccctgcag cagatggccg aggtcaccgg 540
cgaagggttc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaaag ctcatgagc tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
gctgcggaca gtgaaggag aagctgagaa gccagagaga gaggccaaag agcagcacca 720
gaagctgtgg gaagagcagc tggctgctgc caaggcccaa caggagcagg agctggcggc 780
tgatgccttc aaggagctgg atgatgacat ggacgggacg gtctcggtga ctgagctgca 840
gactcaccgg gagctggaca cagatgggga tggggcggtg tcagaagcgg aag ctgaggc 900
cctcctcagt ggggacacac agacagacgc cacctctttc tacgaccgcg tctgggccgc 960

```

```

catcagggac aagtaccggt ccgaggcact gccaccgac cttccagcac cttctgcccc 1020
tgacttgacg gagcccaagg aggagcagcc gccagtgcc tcgtcgccca cagaggagga 1080
ggaggaggag gaggaggagg aagaagaggc tgaagaagag gaggaggagg aggattccga 1140
ggaggcccca cgcactgt caccgccga gccggccagc cctgctgagg aagacaaaat 1200
gccgcctac gacgagcaga cgcaggcctt catcgatgct gccaggagg ccgcaacaa 1260
gttcgaggag gccgagcggc cgtgaagga catggaggag tccatcagga acctggagca 1320
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ccacgacaag ttcatgtcca tgaagtatga gcaaggcacg ggc tgctggc agggcccaa 1560
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gcctgaagca cccaccgaag acgaccatga cgagctctag ctggatggg gcagagaacc 1740
tcaagaaggc atgaagcc ag cccctgcagt gccgtccacc cgcctctctg gccctgcctg 1800
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gggcccaagg ggggctggtc cacattccca ggcccaaca gcctccaaag atgggtaaag 1920
gagcttgccc tccctgggcc cccaccttg gtgactcgcc ccaccaccc cagccct gtc 1980
cctgccacc ctcctagtgg ggactagtga atgacttgac ctgtgacctc aatacaataa 2040
atgtgatccc ccacc                                     2056

```

<210> 265
 <211> 379
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence :primer

<220>
 <221> misc_feature
 <222> (1)..(379)
 <223> 5' terminal sequence. diphtheria toxin
 receptor (heparin-binding epidermal growth
 factor-like growth factor) (DTR) gene.

```

<400> 265
ggttctgtga cccatctgta gtaatttatt gtctgtctac atttctgc ag atcttccgtg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgcc aggcgatttt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctccccgt gtcctctccc 240
tgccaagtct cagaagaggc tgggctt cca tgcctgtagc ttctctggtc cctcaccccc 300
atggcccccag gccacacagc tggagactnc actttncct tgtgtcaaga catttctctn 360
aactcctgnc attcttctg                                     379

```

<210> 266
 <211> 2360
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2360)
 <223> diphtheria toxin receptor (heparin-binding
 epidermal growth factor-like growth factor) (DTR)
 gene.

<400> 266

```

gctacgcggg ccacgctgct ggctggcctg accta ggcgc gcggggctcg gcggccgcgc 60
gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccg 120
ccaggcttgc acgcagaggc ggccggcaga cgggtgcccg cggaatctcc tgagctccgc 180
cgcccagctc tggtgccagc gccagtggc cgccgcttcg aaagtgactg gtgctcgcgc 240
gcctcctctc ggtgcgggac catgaagctg ctgccgtcgg tgggtctgaa gctctttctg 300
gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
gctgctggaa ccagcaaccc ggaccctccc actgtatcca cggaccagct gctacccta 420
ggaggcggcc gggaccggaa agtccgtgac ttgcaagagg cagatctgga cctttt gaga 480
gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
agaaagaaga aaggcaaggg gctagggaag aagagggacc catgtcttcg gaaatacaag 600
gacttctgca tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctccctgcac 660
tgccaccggg gttaccatgg agagagggtg catg ggctga gcctcccagt ggaaaatcgc 720
ttatatacct atgaccacac aaccatcctg gccgtggtgg ctgtggtgct gtcactctgc 780
tgtctctggg tcatcgtggg gcttctcatg tttaggtacc ataggagagg aggttatgat 840
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atgtactcaa gtaccaccaa gggatct gcc attgggaccc tccagtgtct gatttgatga 1380
gttaactgtg aaataccaca agcctgagaa ctgaattttg ggacttctac ccagatggaa 1440
aaataacaac tatttttgtt gttgtgtgtt gtaaattgcct cttaaattat atatttattt 1500
tattctatgt atgttaattt atttagtttt taacaatcta acaataatat ttcaagtgcc 1560
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cagatatcag tgtctccccg tgcctctccc ctgccaaagtc tcagaagagg ttgggcttcc 1920
atgcctgtag ctttccctgt cctcaccccc catggcccca ggccacagcg tgggaactca 1980
ctttcccttg tgtca agaca tttctctaac tcttgccatt cttctggtgc tactccatgc 2040
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ggaacaggga acattggagc tgactgttct tggttaactga ttacctgcca attgctaccg 2160
agaaggttgg aggtggggaa ggctttgtat aatcccaccc acctcaccaa aacg atgaag 2220
gtatgtctgc atggtccttt ctggaagttt ctggtgccat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1.(mac-1) beta subunit) (ITGB2) gene.

<400> 267

```

aggagtcccc cggtgcccc tcaccctgtg gcaagtacat ctctgcgcc gactgctga 60

```

```

agttcgaaaa gggccctnt ggaagaactg cagcgcggcg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagagggac tcagag ggct gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcatct gggaaggctc tgatccacct gagegacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtcc cagtnggaac aatgattatt 420
ccctttttca agagc                                         435

```

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
lymphocyte function-associated antigen 1;
macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
gene.

<400> 268

```

cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgccgc ggact ccagc 60
acaccgaggg acatgctggg cctgcgcccc ccactgctcg ccttggtggg gctgctctcc 120
ctcgggtgcg tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
atcgagtcgg ggcccggctg cacctggtgc cagaagctga acttcacagg gccgggggat 240
cctgactcca ttcgctgcga caccggcca cagc tgctca tgaggggctg tgcggctgac 300
gacatcatgg accccacaag cctcgctgaa acccaggaag accacaatgg gggccagaag 360
cagctgtccc cacaaaaagt gacgctttac ctgcgaccag gccaggcagc agcgttcaac 420
gtgaccttcc ggcgggccaa gggtacccc atcgacctgt actatctgat ggacctctcc 480
tactccatgc ttgatgacct caggaatgtc aagaagctag gtggcgacct gctccgggcc 540
ctcaacgaga tcaccgagtc cggccgcatt ggcttcgggt ccttcgtgga caagaccgtg 600
ctgccgttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg 780
ctggacgcga tgatgcaggc cggcgctgc cggaggaaa tgggctggcg caacgtcacg 840
cggctcgtgg tgttggccac tgatgacggc ttccatttcg cgggcgacgg aaagctgggc 900
gccatcctga ccccaacga cggccgctgt ca cctggagg acaacttgta caagaggagc 960
aacgaattcg actaccatc ggtgggccag ctggcgca ca agctggctga aaacaacatc 1020
cagcccactt tcgcggtgac cagtaggatg gtgaagacct acgagaaact caccgagatc 1080
atccccaagt cagccgtggg ggagctgtct gaggactcca gcaatgtggt ccatctcatt 1140
aagaatgctt acaataaact ctctccagg gtcttcctgg atcacaacgc cctccccgac 1200
accctgaaag tcacctacga ctcttctgc agcaatggag tgacgcacag gaaccagccc 1260
agaggtgact gtgatggcgt gcagatcaat gtccgatca ccttcagggt gaaggtcacg 1320
gccacagagt gcatccagga gcagtcgttt gtcatecggg cgtggg ctt cacggacata 1380
gtgaccgtgc aggttcttcc ccagtgtgag tgcgggtgcc gggaccagag cagagaccgc 1440
agcctctgcc atggcaaggg cttcttgag tgcggcatct gcagggtgta cactggctac 1500
attgggaaaa actgtgagtg ccagacacag ggcggagca gccaggagct ggaagggaagc 1560
tgccggaagg acaacaactc c atcatctgc tcagggctgg gggactgtgt ctgcgggcag 1620
tgctgtgcc acaccagcga cgtccccggc aagctgatat acgggcagta ctgcgagtgt 1680
gacaccatca actgtgagcg ctacaacggc caggtctgcg gcggccggg gagggggctc 1740
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aggaccactg agggctgcct gaaccgcgg cgtgttgagt gtagtggtcg tggccgggtc 1860
cgctgcaacg tatgcagtg ccattcaggc taccagctgc ctctgtgcca ggagtgcgcc 1920
ggctgcccct caccctgtgg caagtacatc tcctgcggc agtgccctgaa gttcgaaaag 1980
ggccctttg ggaagaactg cagcgcggcg tgtcc gggcc tgcagctgtc gaacaacccc 2040
gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc ctacacgctg 2100

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176/292

```

gagcagcagg acgggatgga ccgctacctc atctatgttg atgagagccg agagtgtgtg 2160
gcaggcccca acatcgccgc catcgctcgg gccaccgtgg caggcatcgt gctgatcggc 2220
attctcctgc tggatcatct gaaggtctct atccacctga gcgacctccg ggagtacagg 2280
cgctttgaga aggagaagct caagtcccag tggacaatg ataatcccct tttcaagagc 2340
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aggccgtcag gacccaccat gtctgcccc aacgcgggcc gagacatgg c ttggccacag 2460
ctcttgagga tgtcaccaat taaccagaaa tccagttatt ttccgccctc aaaatgacag 2520
ccatggccgg ccggtgcttc tgggggctcg tcggggggac agctccactc tgactggcac 2580
agtctttgca tggagacttg aggagggctt gaggttggtg aggttaggtg cgtgtttcct 2640
gtgcaagtca ggacatcagt ctg attaaag gtggtgcca tttatttaca tttaaacttg 2700
tcagggtata aaatgacatc ccattaatta tattgttaat caatcacgtg tatagaaaaa 2760
aaaataaaac ttcaat 2776

```

<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

ccaggaccct gaaggtgcta ccagctcctc ttacttgccc agtccccaag aggaagattc 60
aggccagagt cttcccactg cccatgttcg cccttcccac ccattgaaga gcttcgccgt 120
gccagcaatc ccgctccag gacctccac ctatgacct gcattgcaa gcacaccatt 180
actgtcccag caagctctga accatcacat tcaactcagt aagacagcct ccacgggac 240
tctaggaag ggagccggcc tctatgcca gtggttgctt ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt ggccatngg gggaggattt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

gggccggggc gggctgggct ggagcagcgg cgcccgggag ccgagcttgc agcgagggac 60
cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgt 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactcctca gcacccctc 180
cttctggctc tactgcctgc tgcctcgcg gcgcggggcg ccgggcgcgg cggcggccag 240
gagcggctcc gcgcgcagc ccccaggagc cagcattcga acgttccact cattttattt 300
tctggtggag ccgtgggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagccttctc caaaaattga atggaaaaaa gatggaactt ttttaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540
 tcttggaaact attatcagta gaacagcgaa gctcatagta gcaggctctc caagatttac 600
 cagccaacca gaaccttcct cagtttatgc tgggaacgga gcaattctga attgtgaagt 660
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 tgatagagtt atcaaacttc caagtggaa gctgggtatc agcaatgcaa ctgaaggaga 780
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 aagattggta ttgctggcag gtggtagcct gtagatcagt gatgttactg aggatgatgc 1080
 tgggacttat ttttgtatag ctgataatgg aaatgagaca attgaagctc aagcagagct 1140
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 tatggatatt gtatttgaat gtgaagtgc tggaaaacca actccaactg tgaagtgggt 1260
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 caaattgacg tggcgacac ctgcatcaga tcctcacgga gacaacctta cctactctgt 1560
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 gatgcaagta accattcaaa acctaagtc agcgaccgtg tacatcttta gagttatggc 1680
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 gccacctgct ccagccacac aaaaaggga gattactggc tacaagatc gctaccgaaa 2160
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 gaattggcag cctccctctg aagccaatgg caaaattaca gg ttacatca tatattacag 3120
 tacagatgtg aatgcagaga tacatgactg ggttattgag cctgttgtgg gaaacagact 3180
 gactcaccag atacaagagt taactcttga cacaccatac tacttcaaaa tccaggcacg 3240
 gaactcaaag ggcatgggac ccatgtctga agctgtccaa ttcagaacac ctaaagcgga 3300
 ctctctgat aaaaatgc cta atgatcaagc ctcagggtct ggagggaag gaagccggct 3360
 gccagacctg ggtccgact aaaaacctcc aatgagcggc agtaacagcc ctcatgggag 3420
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 caaagatgtg aaacctccag atctctggat ccatcatgag agactggagc tgaaccat 3660
 tgataagtct ccagacccaa accccatcat gactgatact ccaattcctc gcaactctca 3720
 agatatcaca ccagttgaca actccatgga cagcaatata catcaaaggc gaaattcata 3780
 cagagggcag ggtcagagc acagcatgtc tacactggct ggaaggcgag gaatgagacc 3840
 aaaaatgatg atgccctttg actccagcc cccagcct gtgattagt cccatcccat 3900
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 cagtcactc taccacccg gcagcccatg gccattggc acatccatgt cctttcaga 4020
 caggccaat tccacagaat ccgttcgaaa tccccagc actgacacca tgccagcctc 4080
 ttctctcaa acatgctgca ctgatcaca ggacctgaa ggtgctacca gtcctctta 4140

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cttggccagc tccaagagg aagattcagg ccagagtctt ccca ctgccc atgttcgccc 4200
ttccccacca ttgaagagct tcgccgtgcc agcaatcccc cctccaggac ctccccaccta 4260
tgatcctgca ttgccaagca caccattact gtcccagcaa gctctgaacc atcacattca 4320
ctcagtgaag acagcctcca tcgggactct aggaaggagc cggcctccta tgccagtggg 4380
tgttccagcgt gccctgaa g tgcaggagac cacaaggatg ttggaagact ccgagagtag 4440
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aaacgctatc acaacagcat gacgaccttc accaggacct gacttcaaac ctgagtctgg 4560
aagtcttgga acctaacctt tgaacaacag gaattgtaca gactacgaga ggacagca ct 4620
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atggccacct gccttcccct ggtcagcctg gaagaagcct gtgtcgaggc agcttccctt 4740
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tgtaagcttt ttttattatt tttttattat aattattaaa ggcctgactc tttcctctca 5220
tcactgtgag attacagatc tatttgaatt gaatgaaatg taacat tgaa aaaaaaaaaa 5280
aaaaaaaaa aaaaaaa 5297

```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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cagggaattn nttcatnatg gaaaaagaca actgaatgcc ctcaactgaa tgtcttcac 60
ccctcttgcc tgaaatttcc accttcccat aggcctgggga gggagtcagt tccagagcag 120
aggaggggtga cagggttgag gagggacttg tgagagctag aacttgga aatggcctag 180
cccacccttc aaaggggaaa agagggagga acaggggatg aaaagttntc cgcagccttc 240
ccttgaactc tcccctgctg ggggagggag gaggttaaag caagacccc tgcccaggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

```

<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

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```

cgtaacatg agttgggctt ggggcagatg aggtctggctg gcggggcggg cagcatgggt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
ggtctggact ccccatcaga gcacacagac accgaaagaa atggacca ga cactaatcat 180
cagaaccccc aaaataagac ctccccattc tccgtgtccc caactggccc cagtacaaag 240
atcaaggctg aagaccccag tggcgattca gcccagcag caccctgcc ccctcagccg 300
gcccagcctc atctgcccc aagcccaactc atgttgacgg gcagccagct agctggggac 360
atacagcagc tcctccagct ccagca gctg gtgcttgtgc caggccacca cctccagcca 420
cctgctcagt tcctgctacc gcaggccag cagagccagc caggcctgct accgacacca 480
aatctattcc agctacctca gcaaacccag ggagctcttc tgacctcca gccccggg 540
gggcttccca cacagcccc caaatgcttg gagccaccat cccacccga ggagccagt 600
gatctggagg agctggagca attcgccgc accttcaagc aacgccgat caagctggg 660
ttcacgcagg gtgatgtggg cctggccatg ggcaagctct acggcaacga cttcagccag 720
acgaccattt cccgcttcga ggccctcaac ctgagcttca agaactgtg caaactcaag 780
ccccctctgg agaagtggct caacgatgca gagactatgt ctgtgg actc aagcctgcc 840
agccccaacc agctgagcag cccagcctg ggttccgac cgggagacgc 900
aagaagagga ccagcatcga gacaaacgct cgcttcgct tagagaagag tttctagcg 960
aaccagaagc ctacctcaga ggagatcctg ctgatcgcc agcagctgca catggagaag 1020
gaagtgatcc gcgtctggt ctg caaccgg cgccagaag agaaacgat caaccctgc 1080
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gacggcagca cagacccctg gaggtccagg ggggcccgag gcagggtcca aacctgagt 1740
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aggaaagacc aaaaaaaca ccaacaaaa aaaaaaaa aaaaggaaag aaactaacca 1920
acaaaagaga aaacaaaaa taatcacaac agaaaccagc tgcccaaaag gaaccagagg 1980
tgaaaaaaca aaaaaaaa ccaaaaaaa accaaaaaa aaaaaaaacc tctacccct 2040
ctagagcc 2048

```

<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

```

ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaaattatg 60
tgattgggga gattaactct aatctccaca tttatataca gaaagctcca tttgttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gatttatatt ccaactaaaa cactgccatg tacatTTTTT ttcctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

```

<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
gaaaagggtg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
aaaactttgt tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
gcagggtttc tttatactgg tgaaggagat accgtgcggg gcttt agttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atcccaaat 300
tgcagattta tcaacggctt ttatcttgaa aatagtcca cgagctctac aaattctggt 360
atccagaatg gtcagtcaca agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcaggg ttagatata 480
tcagacacca tatacccgag gaacctgcc atgtattgtg aagaagctag attaaagtcc 540
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
tggaacactt gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
gttttgggcc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
ttcccaaatt caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840
tttacttttg ggacatggat atactcagtt aacaaggagc agc ttgcaag agctggattt 900
tatgctttag gtgaagggtga taaagtaaag tgctttcact gtggaggagg gctaactgat 960
tggaagccca gtgaagaccc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020
ctgttagaac agaagggaca agaatatata aacaatatc atttaactca ttcaacttag 1080
gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
atcttccaaa atcctatggt acaagaagct atacgaatgg ggttcagttt caaggacatt 1200
aagaaaataa tggaggaaaa aattcagata tctgggagca actataaatc acttgagggt 1260
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tcattacaga aagagattag tactgaagag cagctaaggc gcctgcaaga ggagaagctt 1380
tgcaaaatct gtatggatag aaatattgct atcgtttttg ttcttgttg acatctagtc 1440
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ttcaagcaaa aaatttttat gtcttaactc aac tctatag taggcatggt atgttgttct 1560
tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
tagcatttgc taccaagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
atctttgaat ttcttgattt ttcagggtat tagctgtatt atccattttt tttactgtta 1740
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attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
tcttttcaga taggcctaac aaatggagct ttctgtatat aaatgtggag attagagtta 1920
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gaaagataga gattgtttt agaggttggg tgttgtgtt taggattctg tccattttct 2040
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aaagcgtatt taatgataga atactatoga gccaacatgt actgacatgg aaagatgtca 2160
gagatatgtt aagtgtaaaa t gcaagtggc gggacactat gtatagtctg agccagatca 2220
aagtatgtat gttgttaata tgcatagaac gagagatttg gaaagatata caccaaaactg 2280
ttaaattgtg tttctcttcg gggagggggg gattggggga ggggcccag aggggtttta 2340
gaggggccc ttacatttgc acttttttca tttgttctg ttcgattttt ttataagtat 2400
gtagaccccg aagggtttta tgggaactaa catcagtaac ctaacccccg tgactatcct 2460
gtgctcttcc tagggagctg tgttgtttcc caccaccac cttccctct gaacaaatgc 2520
ctgagtgtcg gggcactttg 2540

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<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gttttaggaa caagggaata tcttattgtc acgcattcac 120
agtgaaaacc attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180
acaaggcct ggctcctctt cctgtgtact gcccgacttc ctcactttac tgggtccagc 240
ataaagcaga tgtccactgt cttcct caca tgctgtgatc ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggttcgcgtt acttaggaac agcagctctt tttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaatcc tttgggttat agttggaac caggatggga ataaagggat ccagggcac 480
aaatccttc tttccagca actcctgcgg cagataggct ttccggggct taaagagaga 540
cccagctcgg ctcagagcgg acacaatggc gcctccatgc caatcatnct tcatcatttt 600
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660
gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgccctgtca aaccacttct ccagaagac tccctttctt aggtttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
gaattccgcc ggccccaggc agcgtgtgtc ggtcgcctag gctggagaac tagtcct cga 60
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120
ggacctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgaccc 240
ggccaagcat ggggatcagc acgaggtca gcacta caac atctccccc aggatttgga 300
gactgtattt ccccatggcc ttctcctcgc ctttgtgatg cagggtgaaga cattcagtga 360
agcttgctcg atggtaaagga aaccagccct agaacttctg cattacctga aaaacaccag 420
ttttgcttat ccagctatac gatatttct gtatggagag aagggaacag gaaaaacct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgctcat ctttgggtga aaaattgtcg ggtcttctg cagtccagct acaacaaca 600
gcgctttgat caacctttag aggttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttctg aaccagataa aagttcaaga gaagtatgtc tggataaaga gagaaa gcac 720
tgagaaaggg agtccctcgg gagaagtggg tgaacagggc ataacacggg tgaggaaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
tcacctcta gtggccgtgg atggaatcaa tgctctttgg ggaagaacca ctctgaaaag 900

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agaagataaa agcccgattg ccccgagga atta gcactt gttcacaact tgaggaaaat 960
gatgaaaaat gattggcatg gaggcgcat tgtgtcggtt ttgagccaga ctgggtctct 1020
ctttaagccc cgaaagcct atctgcccc ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc ttattccca tcctggtttc caactataac ccaaaggaat ttgaaagttg 1140
tattcagtat tatttggaac acaattggct tcaacatgag aaagctccta cagaagaagg 1200
gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcaactgtgc 1260
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accagtaag atgaggaagt cgggcagtac acaggaagag gagccaggc c cttgtacct 1380
tggtgattga caggactgca gttggctctg gacctgcatt aaaatgggtt tcaactgtga 1440
tgctgtacaa taagatatcc cctgttcttc aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaa 1608

```

<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 277

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ttagattgca tgctattgta tgtctacagg gcatttgaca gcccagagnt aaatccaggt 60
gggacgggat ctaatgatgt cctgtccttc actgtccttg ccacaccag ccacagagat 120
ccaggctttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

```

<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 278

```

gggatctttt tggtctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgctggaag gctgctccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccctccg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

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ccttacacca agttgcacat attccataat aaagtgtgt gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgagggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240
gtatgagacg caggtggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300
ctggggttct tctttcagag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaactttt cggcctggag tgggtgtgtct aagggactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attccccca aaggaggggc 120
ccttggggag gggcctgggc tncccoatgc aaccagcata gccctactg gggccccca 180
tgttacacc taaagcctga aacctgaacc ccantactct gacagaagaa cccaggggc 240
ctgtagccct aagtggtagt aactttcctt cattcaacc acctgcgtct tatactcanc 300
tcanccact gttggctgat ttggatttt tgtggcccca tgtaaggaa cctttaattt 360
ggcattnccc aattgagaat taacctttt gnccgaaca tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe
combined immunodeficiency) (IL2RG) gene.

<400> 281

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gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttctgcagc 60
tgccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttctg accactatgc ccactgactc cc tcagtgtt tccactctgc 180
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttgggaaca 240
gcagctctga gccccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaacccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtgcagta ccggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatggg 660
agaaacgcta cacgtttcgt gttcggagcc gctttaacc cctctgtgga agtgcctcagc 720
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tgctgtctat actcacctca cccactgtg gctgatttg aattttgtgc cccatg taa 1260
gcaccccttc atttggcatt cccacttga gaattaccct ttgccccga acatgttttt 1320
cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttcctc 1380
ccttctctt tccatctacc ctccgattgt tcctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451
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<210> 282

<211> 317

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 282

```
atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagtg aaacccattt taatgcaggt ccagagccaa ctgcagtcct 180
gtccaatccc atagggtaca agggcctggg ctctcttccc tgtgtactgc ccgacttcct 240
catcttactg gggccagca taaagcagga tgtccactgt ctctctcaca tgctgtganc 300
ttggncttag gaggtag 317
```

<210> 283

<211> 358

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(358)
<223> 5' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 283
aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga 120
tccataagtt ggacctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccca gttcccagc tgagagtccc gagagctatt ttcccgaac 240
caatgagaat gaccccgcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358

<210> 284
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. ptk2 protein tyrosine
kinase 2 (PTK2) gene.

<400> 284
gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgccaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240
aagatgttct ctgaccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctgggtg aaaaatcttt ctcataataag 360
tttnaaccac atttggattt ggggttcatt ttttgttttg ttttttttc aatcat 416

<210> 285
<211> 3052
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3052)
<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285
ccggtgtgaa ggccatgagt gattactggg ttgttggaag gaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttctaagag tttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcggccag 300

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatcct gctgacttca 360
ctcaagtgc aaccattcag tattcaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgc ggcaccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctcgagc 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagtgg 600
ccaacagcga aaagcaaggc atcgcgacac acgccgtctc tgtgtcag aa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaga aagaatagaa cttggacgat gtattggaga aggccaat tt ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc gactttggc ggttgcaatt aaaacatgta 840
aaaactgtac ttcgagacgc gtgaga gaga aatttcttca agaagcctgc cattacacat 900
ctttgactg gaattgggtgc agatatataa gtgacctaag tgttgatgcc tgcccagacc 960
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ctggttcaca tggaatcaca gccatggctg gcagcatcta tccagggtcag gcattctctt 1860
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tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca acccatctga 1980
tggaagagcg tctaaccga cagcaacagg aaatggaaga agatcagcgc tggctggaaa 2040
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ctgcagctcc accaaagaaa ccgcctcgcc ctggagctcc cggtcactct ggaagccttg 2160
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tcagccccc tcctactgcc aacctggacc ggtcgaatga taagggtgtac gagaatgtga 2280
cgggcctggg gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
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tggatgcaa aaacttac tc gatgtcattg accaagcaag actgaaaatg ctggggcaga 2640
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ctagccttcc accagcagc aggaattaac cctgtgtcct cagtgcagc cactcacagc 2760
tccaactttt ttgaatgacc atctggttga aaaatctttc tcatataagt ttaacca cac 2820
tttgatttgg gttcattttt tgttttgtt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaaggg ggatggccaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagaggga gagccggaat tc 3052

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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 286
gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagaggga cataccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcctcc 240
atgggcagcc actccattgc tccctccggn ttaccttcac cttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtgggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

<210> 287
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(363)
<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 287
catatctgga caaggcacc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtggtna aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttg 300
ctgtatcttt gcagagatgt ttctgcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363

<210> 288
<211> 1443
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1443)
<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288
gccctcccag tttccgcgcg cctctttggc agctggtcac atgggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggcggggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggcgtagga accggctccg gggccccgat aacggccgc 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttggtgtcgg tgcctatggg acagtgt aca aggccgtga 300
tccccacagt ggccactttg tggccctcaa gagtgtgaga gtcccaatg gaggaggagg 360
tgaggagggc cttcccatca gcacagttcg tgagggtggct ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaagga catatctgga 540
caaggcacc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagggccta gatttccttc atgccaattg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtggtg gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720

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cagctaccag atggcactta caccctgtgt tgttacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggttggt gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg cccagtgcag tgggtgttac ctgagatgga 1020
ggagtcggga gcacagctgc tgcctgaaat gctgactttt aaccacaca agcgaatctc 1080
tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgagc 1140
aatggagtgg ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
gcaatctttg cctttatctc tgaggctatg gagggctctc ctccatcttt ctacagagat 1260
tactttgctg ccttaatgac attccccctc cacctctcct tttgaggctt ctcttctcc 1320
ttccatttc tctacactaa ggggtatgtt ccctcttgct cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

```

ccgcgtgtg tgcgcctaan ctcagngngn ccacccgaga ccccttgagc accaacccta 60
gtccccgcg cggccctna ttcgctccga caagatgaaa gaaaca atca tgaaccagg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcagaaa 180
gaagaagggt gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaa 240
gangttagg gtaacaata tctctggnat tgaagagggt aatatgttta caaaccagg 300
aacagtgat cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

```

<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

```

atgcgacgga caggcgaccc cgctcaggct gactctcggg ggcgagggtc agccaggggc 60
ggctgccctc gggcgaggc gacgtgtct caacctccac ctgcggcgg aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg ttacaaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gcgaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgccaaaac aatctgtgga tggaaaagca 420
ccatttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

```

<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tcctgcttgg nggtggccagc cacatgccaa ggtcccctgc 120
cttctagccc agaatgacgg gactgggcag aacacccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttggagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attccttagag gagccatcct gntccaaggg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgtcct ctcagagagg ggagatctca 360
ctctctgccg gtctgtctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v-fms)
oncogene homolog (CSF1R) gene.

<400> 292
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 24 0
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300
atgggcccag gaggttctgct gtcctgctg gtggccacag cttggcatgg tcagggaatc 360
ccagtgatag agcccagtgt ccccgagctg gtcgtgaagc caggagcaac ggtgaccttg 420
cgatgtgtgg gcaatggcag cgtggaatgg gatggccccg catcacctca ctggaccctg 480
tactctgatg gctccagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540
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caggacgcac tactgcctg tctgtctaca gaccgggtgc tggaaagcagg cgtctcgctg 720
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ggcttcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccttg 840
atgggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900
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cagatcgtgt gtcagccag cagcgttgat gttactttg atgtcttcct ccaacacaac 1020

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aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
ctgacctca acctcgatca agtagatttc caacatg ccg gcaactactc ctgcgtggcc 1140
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ttgaacttga gctctgagca gaacctcatc caggaggtga ccgtggggga ggggtcaac 1260
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cactctcccc tcctccaaac ttcaactcct ccatggatgg ggcgacacgg ggagaacata 3300
caaactctgc cttcggtcat ttactcaac agctcggccc agctctgaaa cttgggaagg 3360
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tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctcaggcccc ttggagcagg atggctcctc taag aatctc 3720
acaggacctc ttagtctctg cctatacgc cgccttact ccacagctc acccctccca 3780
ccccatact ggtactgctg taatgagcca agtggcagct aaaagtggg ggtgtctgc 3840
ccagtcccgt cattctgggc tagaaggcag gggaccttgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
ctctgtccac attaaactaa cagcattaat gc
3992

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<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

191/292

<221> misc_feature
 <222> (1)..(356)
 <223> 3' terminal sequence. friend leukemia virus
 integration 1 (FLI1) gene.

<400> 293
 tttatttagt caaattattt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
 aatatagtta aaaaagtcaa caattacctg caaaattata tataatnnaa tgtctaaaaa 120
 tatgtngctt atatagagca ggaaaatccc tctctccac aagggaaggt ttcgttggtt 180
 tnccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240
 aatgggatta tctttncctt gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
 ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggctata g ggcatt 356

<210> 294
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(465)
 <223> 5' terminal sequence. friend leukemia virus
 integration 1 (FLI1) gene.

<400> 294
 gaccaaagca gtttcttgct aatacacggg gttcagtatg acacagaatc atggacttaa 60
 cccgtcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataataat 120
 tttaggagga ccaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
 tttcacccaa ctggaatttg atggaaagaa ggtt tgtgtg ttttaagacgc caagggcatt 240
 gcagaatccc tctcagtga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
 aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
 attaaattna ctaattttnt tttttttttt ttaaatgatn gacagtggtt ccccggaact 420
 tgggaaangt ttagggggtt ttctaaaccc aagncgattc gcant 465

<210> 295
 <211> 2957
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2957)
 <223> friend leukemia virus integrati on 1 (FLI1)
 gene.

<400> 295
 gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60
 ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120
 taaccgggtc aatgtgtgga atattggggg gctcggtgc agacttgcc aaatggacgg 180
 gactattaag gaggctctgt cgggtgtgag cgacgaccag tccctctttg actcagcgta 240
 cggagcggca gccatctcc ccaaggccga catgactgcc toggggagtc ctgactacgg 300
 gcagccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagtga 360
 ggtcaacgtc aagcgggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

192/292

```

cagcgttagc aaatgcagca agctgggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tcctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtgggccata aaggagtaca gcttgatgga gatcgacaca tcctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgttgtcac acctcagtta cctcagggaa agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
ctcagtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtccctc 900
ccttggaagg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccagaca gcagtgcct agccaaccct ggaagcgggc agatccagct 1020
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ggggaccaac ggggagttca aaatgacgga ccccgatgag gtggccaggc gctggggcga 1140
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ccatccatcc tccatgcctg tcaactctc cagcttcttt ggagccgcat cacaatactg 1440
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cgtgccttca cacttaggca gctactacta gaagcttctt ctactgaag cccatcctgc 1560
acacttactg gatgctttgg actcaacagg acatatgtgg ccttgaaggg aagacaaaac 1620
tggatgttct ttctgttgg atagaacctt tgtatttgtt ctttaaaaac atttttttta 1680
atgttggtaa ctttgcctc ctctacctga acaaaga gat gaataattcc atgggccagt 1740
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atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtaataca cggggttcag tatgacacag aatcatggac ttaaccgcgc 1920
atgttctggt ttgagattta gtgacaaata gaggtgggaa gcttataatc taattttagg 1980
aggaccaaat tcagcggatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
ccaactggaa ttgatggaa agaaggtttg tgtgtttaag acgccaaggg cattgcagaa 2100
tccctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaatgc aaatacatac attcctgaaa gacggggaat taaattacta 2220
attttttttt tttaaatgat gacagtggtc ccagaacttg gaaaagtgt agggatttct 2280
aaactcaagc agattcgcaa gtgctgtgcg cttgtcagac catcagacca gggccaacca 2340
atcagaaggc aacttactgt ataaa ttatg cagagttatt ttcctatatc tcacagtatt 2400
aaaaaataaa taattaaaaa ttaagaataa ataaacgagt tgacctcggc caaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaag taatttgatc atcttttttc 2520
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cctatagctg aaaaaggaaac agggctgttt aagtcactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata tttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaaaagaaga ccagtgtgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

```

<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```
caccccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgctgagcgg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatatcatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tggtttttta gatacaaac ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400
```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```
cgtgtagat tttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaattgga 180
tgcactcaat aaatatTTTT ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtcatccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtggt tgaccctcca cttgccttgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgtgg aacagacaag gccaccntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464
```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

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aaataccaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaaataaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccttt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaatgggt 360
tnaggcctcc ccaacttt 378
```

<210> 299

<211> 317

194/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga ccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgcgcgtg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

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gagtcacagc gctggtgcgc ggagcgggtc accgtcttcg gagcgggttc gccacgcctt 60
tcgccagggc gccacggccc gctgcgcgcg tgcgtgagcg cgccctgcgc gccagggccg 120
ctgcaagggg aggagagcgg ccgcctcagg aggatccctt ttccccaga aattactcaa 180
tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ctttttatgg tcccaggga atctcgatct gaggaatgca gagggcggcc 300
tgtgattgac agaaagagga agtttttga cacagatctg gctcacgatt ctgaagagct 360
atttcaggat ctacgtcaac ttcaagaggc ttgggttagct gaagcacaag ttcctgatga 420
tgaacagttt gtcccaga tt ttcagtctga taacctggtg ctcatgccc cacctccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tcctacaacc cccctctcac ccacccatca 660
gaatcccta tttccccac ctcaggcaac tctgccacc tcagggcatg cccctgcagc 720
tgccccagtt caaggtgtgg gccccgcccc cgcccccat tcgcttcag agcctggacc 780
acagcagcaa acatttgcg tccccgacc accacatcag cccctgcaga tgccaaagat 840
gatgcctgaa aaccagtatc catcagaaca gagatttc ag agacaactgt ctgaacctg 900
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cattgcctgg acaggtcgag gcatggagtt caagctgata gaaccggaag aggttgctcg 1440
gcgctggggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
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195/292

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ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
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cctgaaggca gagtccgagt gccacctcag cgaggaggac accctgccgc tgacccactt 1680
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cattcaggca aacaagggca gtggttttgt ttgtgttttt ggttgttcct aaagcttgcc 1860
ctttgagtat tatctggaga acccaagctg tctctggatt ggcaccctta aagacagata 1920
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atctcgatcg atcatggact actaaatggc ctttacatag aagggctctg atttgcaaa 2160
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aattattctc attgctgtat tatattggaa aagtttttaa caaccaagct aaagctatgt 3180
gaaagttgag ctcaaagtag aggaaaagtt actggtggtg ccttgctgcc tgctctgctg 3240
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gaacctgcca gctgatttga aatactttca cctgcgcag ggccgtatgc atcctgcca 4020
gctgcgttat attctgtact gtgtacaata aagaagttg cttttcgtt a 4071

```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

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nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

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196/292

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagntaaa ggcaaagntt gccctctcag tntccngaag ggaaatggca gcttttcttc 240
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gggtgctgca gagctcgaaa ggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
ncccgagca gctttgcttc cccgactcct nccttttcag gnacccc 407

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

attcgnaca gaggaggagg tggaggaggc cttcccatca gcacagtctg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca ttagaccag 180
gacctaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaata 60
ttaagtttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatttaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa ggttaggtgt tttatcccta ctatacaatt gttattatat 300
agggaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttccggccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

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```

gttatggcgtt cacattcatt gcagtgggat atgggttttta tgtaaaacat ttttagaact 3120
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ctgctcccca ggttcacacc attctcctgc ctgagcctcc cgagtagctg ggactacagg 3300
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taaacttaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
ttctcattga atgcacc 4517

```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced protein 75, 52kd (IFI75) gene.

<400> 305

```

ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcagggttg cactggccac ttgcacagtg ctagtgagga 180
ggctgggcat ctctctgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
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gggctgggag actcaactcag gatctcatcg ctttgcctgg agg atgttcc agggctcact 360
gactcttggg cgacacaagg gaaacagctt ggtttgaagg gggtnnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttcctt ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga cttcctgttt tgctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttcaccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgct atgccataga caagccattt cctttctttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctcacccaa ctgggagagg actttttaac 360
ctgtntctctt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon-induced protein 75, 52kd (IFI75)
gene.

<400> 307
aattccggca tcgctttgct gggaggatgt tccaggctca ctgactcttg gcgcacaggg 60
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tccaggaagg aagaagcact tcagtgaacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcactagcac tgtgcaagtg gccagtgaac 240
acctgatccc ccaaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaaccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctggtcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggttgatc aggttctcctca aaagaaagat gactcaactt 540
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atttaattatt cgagattacg gtgagccttt caggaagcaa tgtgggttga cctgggttaag 1500
ggaaaggctg attacggaaa tgtacacggg ggcgccgaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

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gttannncan tnnatTTTTT aagagagagg caattttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tcctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gttccttcca cctgagagt c tggggagggg 300
ctggtggcag aaggctccct gcaggagggtt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

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cggacccatt caagaaagtc cggaagtctc tggctottga cattgtggat gaggatatga 120
agctgatgat gtccacactg ccaagtctc tatccttgcc gacaactgcc ccttcaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggcttct 240
tgcaggcaa gcccgagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgcccctat gtccagtgcc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

```

<400> 310
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cggggggatg tctcggcgga cgcgtgcga ggatctggat gagctgcact accaggacac 180
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cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
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gcctcatctc agacctgct taggatggg gatgtggcca ggggtgctcc tgtgctcacc 2580
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```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth factor, beta receptor iii (betaglyc an, 300kd)

(TGFB3) gene.

<400> 311

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cccagactca aggagtgtgt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa tttgcacctt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaatg tcttaatggc 360
aaattttcta tttcttacag ggntacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
```

<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

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taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt tttccaatct cagcactgtc ttgngngaatt 180
tggtgacact attcagataa ccaactggag accgacagat ttgcatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
```

<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

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tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg ctttcaaact 60
gaaagaaccg catgagcctg acggcgcgat gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
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ggtgacactg gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagc agaggcacia ctgggctgcc acaggaggtg 540
```

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catgtctctga atctcgcact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
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gtcaaaaatc tcatcctgat cttgaagtgc aaaaagtctg tcaactgggt gatcaaatct 1200
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ctggattttg gttcccttgc aaagacagag tgaatttcag tataaagatc acccgttgta 3060
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aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtataacc 4200

tccttgtt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacott tccctaatac ttnatnggtn acctctaggc ctgtgtgcgg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttga gggcaggtc tggcctttcc 180
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agctcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccaggtt tccagccagc gggacaaant 360
ttccccatgt tcgtttgtgt attggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcggtg gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggtcctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttcacccac ctggcttga tcaacacccc ccgaaagag 240
ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

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<221> misc_feature
<222> (1)..(937)
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316
cgcgggcccca gggctcactt ggcgctgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaaagc 120
cagcccctga cttcaaggcc acagcgttg ttgatggcg cttcaaagag gtgaagctgt 180
cggactacaa aggggaagtac gtggctcctt ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtcggg cgtctcggtg gactc tcagt tcacccacct ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc cecttgaaca tccccctgct tgctgaactg accagacgct 420
tgtctgagga ttacggcgtg ctgaaaaacg atgaggcat tgcttacagg gccctcttta 480
tcctgatgg caagggtgtc cttcgccaga tcactgttaa tgatttcct gtgggacgct 540
ccgtggatga ggctctgcg ctggtccagg cttccagta cacagacgag catggggaag 600
tttgtccggc tgcttggaa cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatattt ctcaaacac aattagctg gctaaccgat agtgagctt tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgaccagg 780
aaaggccaga cctgccctc caaatccac agtatggag cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgcctc cccaagccc accagccgc 900
acacaggcct agaggtaac aataaagtat tagggcc 937

<210> 317
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317
gctagacaca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gcccgctccg tgccagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcaact ccggtggtca cctgtactcc cagctgcact gctta cacgt 240
cttccttctg cttcacctac cccgaggctg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttcctc tgactcgttc agctnaccna cgggtgctggc 360
cctgtgaggg gccaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451

<210> 318
<211> 2084
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2084)
<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.

<400> 318
aaccgcatct gcagcgagca actgagaagc caagactgag cggcgggccg cggcgcgagcg 60
aacgagcagt gaccgtgctc ctaccagct ctgcttcaca gcgcccacct gtctccgcc 120
ctcggcccct cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgagc gtcac ctc cgctgcagca gcgcgtccc ggccgggat agcctctctt 240
actaccaact acccgagac tcctctcca gcatgggctc gcctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtcca acttcattcc cacggctact gccatctcga 360
ccagtcgga cctgcagtgg ctggtgcagc ccgcccctgt ctctctgtg gcccac gc 420
agaccagagc ccctaccct ttcggagtcc ccgcccctc cgctggggct tactccaggg 480
ctggcgttgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaaggga aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcgaga 660
cagaccaact agaagatgag aagtctgctt tgacagccga gattgccaa ctgctgaagg 720
agaaggaaaa actagagttc atctggcag ctacacgacc tgctgcaag atccctgatg 780
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ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
ttgatgactt cctgttcca gcatcatcca ggccagtg ctctgagaca gcccgctccg 1020
tgccagacat ggacctatct gggtccttct atgcagcaga ctgggagcct ctgca cagtg 1080
gtccctggg gatggggccc atggccacag agctggagcc cctgtgcact ccggtggtca 1140
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actcctccc cagctgtgca gctgccacc gcaagggcag cagcagcaat gaggcttct 1260
ctgactcgtc cagctacccc acgtgctgg ccctgtgagg gggcaggga gggaggcag 1320
ccggcaacca caagtgccac tgcccgagct ggtgcattac agagaggaga aacacatctt 1380
ccctagaggg ttcctgtaga cctagggagg accttatctg tgcgtgaaac acaccaggct 1440
gtgggcctca agcattgaa agcatccatg tgtggactca agtccttacc tctccggag 1500
atgtagcaaa acgcatggag tgtgtattgt tcccagtgac acttcagaga gctggtagt 1560
agtagcatgt tgagccaggc ctgggtctgt gtctctttc tcttctctct tagtctctc 1620
atagcattaa ctaatctatt gggttcatta ttggaattaa cctggtgctg gatattttca 1680
aattgtatct agtgcagctg attttaacaa taactactgt gtt cctggca atagtgtgt 1740
ctgattagaa atgaccaata ttatactaag aaaagatacg actttattt ctggtagata 1800
gaaataaata gctatatoca tgtactgtag tttttcttca acatcaatgt tcattgta 1860
gttactgac atgcattgtt gaggtggtct gaatgttctg acattaacag tttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatattt 1980
tattttattt tttctacct tgaggtcttt tgacatgtg aaagtgaatt tgaatgaaa 2040
atttaagcat tgtttgctta ttgtccaag acattgtcaa taaa 2084

<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

ctgcaaagcc aatcaagaag tgttgaagg aaaaagtgt aaagttatct ttgcatattt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cattctctc 180
ttccctaata gctacaant gatacagtac gcaacagctc acttgaaagt gctagantca 240

<210> 320

207/292

<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 320
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg cccagtcctta 120
ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggcttttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctcgtt aacatggccg cagantcctt cacatccatt gcttacaaan 420
acaccctctt gcttgatggg gttggnnttt tgactat 457

<210> 321
<211> 1946
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1946)
<223> retinoblastoma -binding protein 7 (RBBP7)
gene.

<400> 321
gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctgagacctc ggtacccgcg agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc tttcgacagt 180
ggggagtgtg acgcgcttgg gaaaggcagg agcgcacgcg gtcgggctgc tcttgctaa 240
cgagaggagt ccgaggcggc ggcgaggggc gaacgaccgc acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg cccagtcctta 420
ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggcttttg ttctgtaaca ggaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttggttttt gactatacaa aacaccctgc taaaccagac ccaagtggag 780
aatgtaatcc tgatctcaga ttaagagtc accagaagga aggctatggt ctctcctgga 840
attcaaattt gagtggacat ctccaaagt cactctgatga ccatactgtt tgtctgtggg 900
atataaacgc aggacaaaa gaaggcaaaa ttgtggatgc taaagccatc tttactggcc 960
actcagctgt ttagaggat gtggcctggc acctgctgca cgagtcattg tttgatctg 1020
ttgctgatga tcagaaactt atgatatggg acaccaggtc caataccacc tccaagccga 1080
gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcattcaat ccctacagcg 1140
aatttattct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaattaaa actccatacc ttcgaatctc ataaagatga aattttccag gtccactggg 1260
ctccacataa tgaaactatt ctggcttcaa gtgggtactga ccgccgcctg aatgtgtggg 1320

208/292

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atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cactgtgcta agatttcaga ttttagctgg aacccaatg 1440
agccttgggt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccga aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagtg agctgttgcg tactgtatca tattgtagct 1740
attaggggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtcctca ttttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946
```

<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

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tatagaaatt ctttattatt agacaaaaat agactctctt ttttccccta ttcattgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccacccct ctcccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatcccct gggagggtg 180
acgttctcct gcagggtggg ctgcctgata tccttcgggg ctcaactgct gatgcctcct 240
caccctcac acaccatct ctgccatctg ctcacatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365
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<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

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tcaagggtcg cccagtgag cctactttg gcagcctgtc cgccttggtc tccagcact 60
ccatctccc catctccctg cctgtctgcc tgcgcattcc cagcaaagat cctctggaag 120
agaccccaga ggctccagt cccaccaaca tgagcacagc gncagacctc ctgcgtcagg 180
gtgctgcctg caggtngctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g ccccccccg acaccagctg 300
ttgtccactt caaggtgtca gccagggca ttnacactga cgggacaacc aaaggaagct 360
cttnttttc gccgccatta tccagtggaa cagcatcacc 400
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<210> 324
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 5' terminal sequence. atp-binding cassette,
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
nttcggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60
attcttccca gcagcgacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120
agcgcagagg atcagccttg cccgggcctt gtatagtgc aggagcatct acatcctgga 180
cgacccctc agtgcccttag atgcccatgt ggaanccaca tncctcaata gtgctatccg 240
gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300
actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcacccntg 360
gagggaantg atggatttta aatggtgatt atggttacct ttttaattaa cntgtgtgtg 420
ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
ttcacagtt 489

<210> 325
<211> 5838
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5838)
<223> atp-binding cassette, sub-family c
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325
ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcggtt gtcctggagc 60
aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggtatagaa 180
gtgtgagggg gagaaccagc acttctggga cgcacagaga cagtgaagat tccaagtta 240
ggagaactcg accgttgga tgccaagatg ccttggaac agcagccga gccgagggcc 300
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<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

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tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttncct tgattgtcaa 300
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<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

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<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
 (CDH1) gene.

<400> 328

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<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

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<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

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<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
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<400> 330

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cagccaagcc tctccactcc tctcactttt tctgggccct tttttccact tcttctactt 1320
tcccagctc tcccacctt gggggt gggg ggcggtttt ataaataaat atatatatat 1380
atgtacatag gaaaaaccaa atatacatat ttattttcta tggaccaacc agattaattt 1440
aaatgccaca ggaaacaaac tttatgtgtg tgtgtatgtg tggaaaatgg tgttcatttt 1500
ttttggggg ggtcttgtgt aatttgtgt ttttgggggt gcctggagat gaactggatg 1560
ggccactgga gtctcaataa agctctgcac catectcgt gtttcccaag gcaggtgggtg 1620
tgttgggggc ccttcagac ccaaagcttt aggcattgatt ccaactggct gcatatagga 1680
gtcagttaga attgtttctt tctctcccc tttctctccc catcttggct gctgtcctgc 1740
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ttttacaaat gcagtttatc cctggttctg aggagcaagt gcagggtgga ggtggcacct 1860
gcatcacctc ctctctttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920
ttttttttt tctctgtgtg tgtggccttt gcatcattta tcttgtggaa aagaagattc 1980
aggccctgag aggtctcagc tcttgagga gggctaaggc ttttagcattg tgaagcgtg 2040
caccaccacc aaccttacc tcaccgggga accctcacta gcaggactgg tgggtggagt 2100
tcacctggg cctagagtgg aagtgggggt ggggttaacct cacacaagca cagatcccag 2160
actttgccag aggcaaacag ggaattccgc cgatactgac gggctccagg agt cgtcgcc 2220
acactcg 2227

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(254)
<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgccgat actcggttgg ggattataat 180
tccttccagg gaccagcag ttgtgggtaa agcaggcaag tgggcccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(362)
<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
gccatggncg tggtgctaca cgatggaccc aaggacccca t tcgactact gtgccttgcg 60
acgtctgcgt gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagaggggtg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
tgccggnggt ctctagttaa ggagcagtn gatactgactn cccggaagtg cttctcctcc 300
tnccatatnc ctctcacggg ctatgaggta tggttngggc ancctttttc cagaaccac 360
ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2219)
<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

216/292

<400> 333

```

agccagaagg atgggggtggc tccactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct 120
gctacatgcg gtgggtcccc ggcccttgga ggaggatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggaactgoc ggccctccac tacaacgtga gcagccatgg 240
ttgccaaactg ctgccatgga ctcaacactc gcccacacg aggtgcggc gttctgggcg 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atggggttgg 360
gtaccggggc accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggcttgaag agaacttctg 480
ccgtaaccct gatggcgac c cggaggtcc ttgggtgtac acaacagacc ctgctgtgcg 540
cttcagagc tgccgcatca aatcctgccc ggaggccggc tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcggtag accgcacgga gtcaggggcg gagtccagc gctgggatct 660
tcagcaaccg caccagcacc ccttcgagcc ggccaagtgc ctgaccaag gctctggacga 720
caactattgc cggaaatcctg acggtccga gcggccatgg tgctacacta cggatccgca 780
gatcgagcga gaggttctgt acctccccg ctgcgggtcc gaggcacagc cccgccaaga 840
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caccactgcg ggcgtacctt gccagcggtg ggacgcga a atccgcgac agcaccgatt 960
tacgccagaa aaatacgcgt gcaaagacct tcgggagaac ttctgcccga accccgacgg 1020
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gacgccgcac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgcccg aaccagatg gggatagcca tgggcccctg tgctacacga tggaccaag 1320
gacccattc gactactgtg ccctgcgacg ctgcgctgat gaccagccgc cat caatcct 1380
ggacccccca gaccaggtgc agtttgagaa gtgtggcaag aggggtggatc ggctggatca 1440
gcggcgctcc aagctgcgcg tgggtggggg ccatccgggc aactcaccct ggacagtcag 1500
cttgcggaat cggcaggggc agcatttctg cgggggggtct ctagtgaagg agcagtggtat 1560
actgactgcc cggcagtgct tctcctcc tg ccatatgcct ctacggggt atgaggatatg 1620
gttgggcacc ctgttccaga acccacagca tggagagcca agcctacagc ggggtcccagt 1680
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tccagggacc aagtgtgaga ttgcaggctg ggtgagacc aaaggtagcg gtaatgacac 1860
agtccataat gtggccttcc tgaatgttat ctccaaccag gagtgttaaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggaactg ttggcccctg tgggggacctg 1980
tgagggtgac tacggggggc cacttgccctg ctttaccac a actgctggg tcctggaagg 2040
aattataatc cccaaccgag tatgcgaag gtcccgctg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggt catgagactg ggttaggcc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219

```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```

gaaaggaagg caaactctgc cnccc gctca gagtcccccc aaccctcact gtttcccgtt 60
gccattgatg gggagggttca cgtactcagg ggaggccagg naggcntgna gcttggggcg 120
ggcactgagg cggccacat atgctgagag cagggggaac gcatccagc agccagggtc 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggttctcaa aaggcttcag 300

```

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ttgccccgggc agtgccttca catagtcac cttgcccccc tcatagtgtg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggctg 420
nctcctttt t 431

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335
nattcgccac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccatcctgcg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336
ggagtttctc cgccgcagtc ttgccacca tgccgcccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatac 180
ggcagctccc caagttccag gacggagacc tcacctgtta ccagtcctcc accatcctgc 240
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tgatgctgtt cccctgctc tcagcatatg tggggcgccct cagcgcccg cccaagctca 600
aggccttccct ggctccctcct gactacgtga acctcccat caatggcaac gggaaacagt 660
gaggggttggg gggactctga gcgggaggca gaggttgcct tcctttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtga 300
tccnggggtt ttcttagggt aggctgagga ctcaggggct tatctcacct tctcaggaat 360
gctttttgaa gg                                     372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca ttccggtgac ttccgcatca ggaaggctag agttaccagc agcatcaggc 240
cgccacaagt gctgtctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtccctggaa ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtgtggt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttgttcac ctgg ggggcc 480
ttccaggtag ggcctttttt aagtggga                                     508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```

tttttttant caaaagtttg aaattcaagt aactttatit aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctaggttaa ctagaccaga tctgactt tg gactttatitc tttaaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcaggata tgctgggcàt cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgncttt gggggngggc aggtaggtnt tttaggtgtc ccntatccc 420
ganttttata ctctncaccg gggggg 445

```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```

gctccagcgt tgtaaacctg cagagatgga ctgcgtccac gtctcttttg tgcagctcac 60
cctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tgggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagtt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437

```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```

aggctctcagc cggctcgtgc gacgttcgcc cgctcgctct gaggtctcctg aagccgaaac 60
tagctagact ttctctcttc ccgctgcct gtacggcgtg tgttgccact ccgccaccat 120
gttcgaggcg cgcctggctc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag tccagcgggt gtaaacctgc agagcatgga 240
ctcgtccac gtctcttttg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

```

220/292

```
attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc tttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa octagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaattttaat aaagttactt gaatttcaaa c 1231
```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 342

```
tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatatatt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aagggttaagt gttctcgggt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcc agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac 383
```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 343

```
gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcatct ttgtcctaac atgagtgtt gtaacaaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg ttaaatgctt ccttccctt cccacatata atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttaggtt aatggggtca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcc tgttaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctct gtattttgct gggatgtctg gggtaggga ggccttacct ataggggntg 480
ggg 483
```

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaacat tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
gattttttaca tcattacaca gatattgcat ttccattagt tgtatcattg ttataaactg 240
gtatatgtct cgagtccacg gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaatca 420
tgactgggtat tgttttgaat gccatttgcc tggagagggt ttgatattgt acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
ctggcagtgcc ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600
cacataccctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggtgtgtg cactcagctg tggacgttcc 720
caccattcaa gagaagtga atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780
tgcccaattg cttctccaca ataccgtgat tttctatgga gcagacagtg agcaagctga 840
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaaagaa gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatcac agtcaacatt catcggctgc acgtgaagcg 1140
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
aggagattt tggaaatcta agaattgagga ccgaggtgag gaagaggcag aatccagtat 1260
ctctccacc agtaatgagc agctaaaggc cactcaagaa ccaagagcaa agaaaggacg 1320
acgtaatcaa agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaataacca cgatgcctca gcc atcgaa aaagtctccg tgtcaactca 1440
gacaaagaag ttaagtgcct cttcaccaag aatgctgcat cggagcacc agaccacaaa 1500
cgacggcgtg tgtcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560
agaccggatg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctgcgt tctgaaatgg aagaagaaaa gagacaagct gtaaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800
gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920
ccgaaaaga tgaagctggc ctttcccgga gtcaccccgga tgattactct tttcagacac 1980
agcgggtttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcagggg taaaagttaac atcagtggag ggtattatct taaataaatt 2160
ttaattgaga atttgttgca ttttcagcaa attttaaaac atttttaggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa acagggtgaa tacaagtgtg tttacaaaag 2 280
aaacatttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
ctgttcaaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460
gggttgacac agcagggcta gtcctgcata tttttt ctta aatatttccc aattgtgttt 2520
ttcattatct cttttcaata tataactttt ataacaaatt attagctttg atcttgtagt 2580
ttaaaattgc agggaactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640
tttaaatctt aaagtttgcc acatttcatc tttgtcctaa catgagtgtc tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix

metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcatgcagca tcttgagtgg tagcgtcgat ctgagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccc ggtgctgggg tggaaacgcc agtagtccct 120
gcctcgggaag aagtagatct tgttcttctc gggaccccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggaactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttgga agaaccaaat gtgggcccgg cttaccacagc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca
```

363

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gccccggggc ggatggctcc ggccgcttg ctccgcagcg cggccgcgcg 60
cgccctcctg cccccgatgc tgctgtgtgt gctccagccg ccgcccgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtag cccgg cacctgcccc tgccacgcag gaagcccccc ggccctgccag 240
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gataccttcg ttcccatggc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggtg tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttcg ccagggtactg gcatggggac gacctgccgt ttgatgggcc 540
tgggggcatc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcaggtggc 660
agcccatgaa tttggccacg tgctggggct gcagcacaca acagcagcca aggcctgat 720
gtccgccttc tacaccttcc gctaccact gagctcagc ccagatgact gcaggggcgt 780
tcaacaccta tatggccagc cctggcccac tgtcacctcc aggaccccag ccctggggcc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cggctctccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgccctc gtgggggcca gctgcagccc ggctaccacg cattggcctc 1020
tcgccactgg cagggaactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccgg cgtgtagaca gtcccgtgc c ccgagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggetat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc ccggtctcgt 1440
gggtcctgac ttctttgggt gtgccgagcc tgccaacact ttctctgac catggcttgg 1500
atgccctcag ggggtgctgac ccttgccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
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gtagcaccat ggcaggactg ggggaactgg agtgtccttg ctgtatccct gttgtgaggt 1860
tccttcagg ggctggcact gaagcaaggg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggctgtaggg caggggcact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggggtattct catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctcaaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcggggct gtggccagnt tgcctcacgg aggtgcaggg aggctggggc ctactagggt 240
canctggagg agcacggact gccctgccgg cag 273

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```

224/292

```

cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagaggg 300
gagcttggtt tccagccngg tgaagnacca                               330

```

<210> 349
 <211> 1168
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1168)
 <223> hypothetical protein mgc13071 (MGC13071)
 gene.

```

<400> 349
aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggccctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgtttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag cttcctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tctcaagtc actggtggct cgctttgatg ctggagaact aatcaccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctcattctgg 600
acgacgtgtc tttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgagggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggacg gccagagcga 780
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actggggcac agccccgatg attcgtaaca ccacctttcg 960
ccctcaccac agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168

```

<210> 350
 <211> 315
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(315)
 <223> 5' terminal sequence. interleukin enhancer
 binding factor 2, 45kd (ILF2) gene.

```

<400> 350
ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggtc gaggaaaatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt cnggctttg agc cctcaca 240

```

225/292

ccnnggatnc ttgaactact aggnccattat gctgtgatga acaacccac caganagcct 300
 ttgcnctaa acgtt 315

<210> 351
 <211> 1552
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1552)
 <223> interleukin enhancer binding factor 2, 45kd
 (ILF2) gene.

<400> 351
 cggttggtgc ggccctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
 ggtcgtggtg ggccgttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
 ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180
 cctgatgaaa cttcccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
 tctgctgaac aggcattctat cctttctctg gtgacaaaa taaacaatgt gattgataat 300
 ctgattgtgg ctccagggac a ttggaagtg caaattgaag aagttcgaca ggtgggatcc 360
 tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgt gatactcaag 420
 attctgccaa cggttgaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
 gcacaggatc cttctgaagt tttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
 tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600
 gatccagaac tccatttggg tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
 gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
 aaggacttga ggattcgttt tcttggttgg gagccctca c acctggat ccttgacctg 780
 ctaggccatt atgctgtgat gaacaacccc accagacagc ctttggccct aaacgttgca 840
 tacaggcgct gcttgcatg tctggctgca ggactgttcc tgccagggtc agtgggtatc 900
 actgacccct gtgagagtgg caactttaga gtacacacag tcatgacct agaacagcag 960
 gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020
 aagatccttg gccaggaggg tgatgccagc tatcttgcct ctgaaatctc tacctgggat 1080
 ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
 gaggaagaag aggagaatac agaaaagaac acctcaagga gaggaagaag aaagcatgg a 1200
 aactcaggag tgacattccc ttactcctt ttctaccca agggaaagac tggagcctaa 1260
 gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320
 aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
 tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
 taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500
 aatgttaagt gtctggaat tttttttct aagaaaaact attaaagtac tt 1552

<210> 352
 <211> 396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(396)
 <223> 3' terminal sequence. hypothetical protein
 flj11307 (FLJ11307) gene.

226/292

<400> 352

ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
ggtactggag gtttc agttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcac 180
aaagcctggt ggatatccca ttgcttgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

tcgatgaaag atcctccgga cttattggac aggcagaaat gccgaacgc cttggcgtct 60
cttcgacatg ccaaattggt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120
ctccgcattc tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagacctt gggcgctggg 240
gaggccttga gacgagtaat ggagtgtttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagacca acag atgtct tgagctatat gaccatccag 360
caaaaagaag atattaccca cagtgcacag catgcactca gactatcagc ctttggccag 420
atttacaagg tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga ccccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc cccgttcatg cccagctctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggacat ccaagaaaac agca aaactt 780
cacgtagcgg tgaaggattt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaaatcagat aatgaaagta aaaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgctt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg cagggtccaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaaggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agagggaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg tttaaccaag agaattggtc tgttac ccgt tatgaaattt 1440
ccaacatata ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaaag 1740
tctagcagtt caaagttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgac acaataaac tgctttgtg taacacag 1858

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v -myb avian
myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaaccccag cstatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaac ntacaacgag 240
gt                                     242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene
homolog (MYB) gene.

<400> 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcgggaggc 60
ggcaccocgg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccccg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg ctteccaagt ctggaaagcg tcacttgggg aaaacaaggt 240
ggaccgggga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaaagtta tgccaattat ctcccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccttgag ctcatcaagg gtccctggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacggtccga aacgttggtc tgttattgcc aagcacttaa 480
aggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaagctac tgccctggac aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcgggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatggggt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagccact gttaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcattgt ccataccctg 900
tagcgttaca tgtaaatata gtcaatgtcc ctccagccagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgctacc aacacagAAC cacacatgca 1080
gctaccccg gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagtg 1140
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tgataatgt taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaat gccttcttta acttccaccc 1380
ccctcattgg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaa 1440
ctcaaaagga aaatactgtt tttagaacc cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaactg cacttgcagc tcaagaaatt aaatacgggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatattctt acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcatcct gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcat tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgttgt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gattttttaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctggtatttt 2340
aaaggtacca acagatcagt attttttcct gtgatgggtt ttttgaaatt tgacacatta 2400
aaagtgactc cagtatttca cttttctcga tcactaaaca tatgcatata tttttaaaaa 2460
tcagtaaaag cattactcta agtgtagact taataccatg tgacatttaa tccagattgt 2520
aaatgctcat ttatggtaa tgacattgaa ggtacattta ttgtaccaa ccattttatg 2580
agttttctgt tagcttgcct taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
tatttttatt cagtaattta attttgtaaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggtcttagcc tgtagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgttaggt aattgactat gcactagtat ttcagacttt ttaattttat 2820
atatatatac atttttttct cttctgcaat acatttgaaa acttgttttg gagactctgc 2880
attttttatt gtggtttttt tgttattgtt ggtttataca agcatgcgtt gcacttcttt 2940
tttgggagat gtgtgtgtt catgttctat gttttgttt gtgtgtagcc tgactgtttt 3000
ataattggg agttctgat ttgatccgca tcccctgtgg tttctaagt tatggtctca 3060
gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

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gtagttaa at gcagaaagtc ggttttttcc cacccttttc ctctttttac acggcaagta 60
aagctcactg gcctgggagtg tgctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgcctga gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaaatt tcccacaaga atancctttc 360
tgctcanct 369

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<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
nucleic acid binding protein) (ZNF9) gene.

<400> 357
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggctgcgctc cgagtctccg 60
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccaactggggc cgggaatgtc ctactgggtg aggccgtggg 180
cgtggaatga gaagccgtgg cagaggtggg tttacctcgg atagagggtt ccagtttggt 240
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctggtcactc tgccaaggat 300
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgctgtctaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttggg agaattcgga 480
cacattcaaa aagactgcac caaagtgaag tgctatagggt gtggtgaaac tggtcagtga 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcagggcac 600
cttgcacggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgccttcct 660
ttttctgatt gatggttgta ttattttctc tgaatcctct tcactggcca aaggttggca 720
gatagaggca actcccaggc cagtgaagctt tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaaacc gactttctgc atttaactac aaaaaaagtt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaaccc ctttccgtg ccactggtga atagggattg 900
atgaatggga agagttgagt cagaccagta agcccgtcct gggttccttg aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataaa catcaagtaa 1080
catctgtatc aggccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
atgcgtgtta atggctgttc gagagaaatc ggaataaaaag cctaaacagg aacaacttca 1200
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagttagca taatttggag 1320
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat ttttgtatac 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaaag tcaga tggaa 1440
agagcaactg aagtcttaga aaatagaaat gtaattttta actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60
tcagatatatt aaatgagcac caaacactac aaagtgaac caacatgggt ctattaaaaa 120
ctcncctttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaatataa aaatctgcaa atgccatata ttcatatcta ggctattctt cncatatagg 240
catgtcatta gatagacttt ctttctatct tttccngagg natTTTTTTT nggtttacnt 300
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaattgggag cngcaagtat 420
gtggc 425

<210> 359

230/292

<211> 232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(232)
<223> 5' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 359
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
<211> 1431
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:prime r

<220>
<221> misc_feature
<222> (1)..(1431)
<223> camp responsive element modulator (CREM)
gene.

<400> 360
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
tgcaagttagc tgagatcagg caccagaaga ggctcccag ctgtaactct agtgcagtta 180
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
cagtcacag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
gaatcagaaa gtgtaattga ttctcataaa cgtagagaaa t cttttcacg aagaccctct 360
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
atatacaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540
tctaaccag gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600
gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
cagttctttg tcccaggcag ccaggttgtt gttcaagctg ccactggtga catgccaaact 720
taccagatcc gagctcctac tgctgctttg ccacaggag tggatgatgc tgcacgccc 780
ggaagtgtgc acagtcccca gcagctggca gaagaagcaa cacgcaaacy agagctgagg 840
ctaataaaaa acagagaagc tgcccgggag tgcgcagga agaagaaaga atatgtcaaa 900
tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
tttactctaa tcaaggcagg agatgcagca gtccacttta ttgccatgtg gacttgtggg 1080
aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140
tggtgttcca ggatgtgga tgacagctga tcacacttac cgagcttact ttgatctggt 1200
tgtcaatagc atgcaaaaaa tgctttgttt gccctttgct tctgcttttt ttgagggaag 1260
ctgccaaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
cagtgctgga agtcagaaac aagaagctta tagaggaact tgaaacctg aaagacattt 1380
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca ggtgaagct 60
gtaatttttc aaaaacagta aaagctggtt tctcctaaac tattttcctt gtggtagtag 120
agatcagtg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacaggctct ccgctgttcc actgggtcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gagggttgta cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggctccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gaggtactgg gggaactgat gggggaactt tcatac cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta gcggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgct g gcncttaagg 240
tgaataaggt ggtggtgact gttctgcaga gagtttctca taagcagggt gagcattggg 300
aaccacaggt tcacagtttt tctctgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363
 attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
 tctatggtta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
 ggatcggcat cctgacagtg atcctgggag tcttactgct catcggctgt tggatttgta 180
 gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
 cttacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
 agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
 cagaacagtc 370

<210> 364
 <211> 1524
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1524)
 <223> melan-a (MLANA) gene.

<400> 364
 agcagacaga ggactctcat taaggaaggt gtctgtgcc ctgaccctac aagatgccaa 60
 gagaagatgc tcacttcato tatgtttacc ccaagaagg gacggccac tcttacacca 120
 cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
 tcggctgttg gtattgtaga agacgaaatg gatacagagc ctgtatggat aaaagtcttc 240
 atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggtt gatcatcggg 300
 acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
 cttatgagaa actctctgca gaacagtcac caccacctta ttcaccttaa gagccagcga 420
 gacacctgag acatgtgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
 tctaattgtc tcctttggaa tgggttagga aaaatgcaag ccactctctaa taataagtca 540
 gtgttaaaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
 attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
 gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggattcttg 720
 gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttctga 780
 accttgaccg acatgaactg tacacagaat tgttccagta ctatggagt ctcacaaagg 840
 atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
 agcaatgtct ctttgtgtct taaaattcta ttatactaca ataatatatt gtaaagatcc 960
 tatagctctt tttttttgag atggagtttc gcttttgttg ccag gctgg agtgcaatgg 1020
 cggcatcttg gctcaccata acctccgctt cccagggtta agcaattctc ctgccttagc 1080
 ctctctagta gctgggatta caggcgtgag ccactatgcc tgactaattt tgtagtttta 1140
 gtagagacgg ggtttctcca tgttggtcag gctgggtctca aactctgac ctcaggtgat 1200
 ctgcccgcct cagcctccca aagtgtgga attacaggcg tgagccacca cgctggctg 1260
 gatcctatat cttaggtaag acatataacg cagtctaatt acatttcact tcaaggctca 1320
 atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
 aataagtaaa agctactatg tactgcctta gtgtgatgc ctgtgtactg ccttaaatg t 1440
 acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
 aatcataaag gatcagagat tctg 1524

<210> 365
 <211> 556
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggt aggccttttat tttctcttat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgtagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttgcgagttg aacaatgac actgatcaca aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540
gggnggggat aacc cc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60
cgtcagcaca gcatctttgg agatccgaag aagatcgta cagaagagtt tgtgcgcaga 120
gggtacctga ttataaacc ggtgcccggt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacg tggatcagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcggga cgatgatgca 300
gaggttgagg ctatccctcaa ttcaggtgct aggggttatt ccgcccctta agtagatctg 360
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta ccccaaagg agtagatg nc 420
aaggggccct aagttgcaaa atgatgtoga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcg gcaagtgtcg gcggcggtcg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180
cagcggcagc agcttct tac ggtataaagc tgttgcttcc tgaagaggct acaagcatcc 240

234/292

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac cccggaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggctctac caccctgaa 480
gaagcctcga gcaactgcca agcacaaaag ctttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcacatggg caacagcgcc 600
aaggaagctc tggcttggaag agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag agggtagctg 720
atttataaac cgggtgcccc tagcagtcgg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgcccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtag cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtagt cagtga tcac 1080
tggtcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttcgtttgtg tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtgca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttcggattgc ttatca 1476

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<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaaatat caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcacaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggt tcccaa gagt agccatggtt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttoca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttconaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 369

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ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa ttgtctctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
gacctacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa gggttgctta ctaagtttct gagtggcgga gtgnccaaac ctagggagct 360
agcagttccc attcagggca aacaagnggc agtgnggtt gtt ttgtgtt tttt 414
```

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370

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ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249
```

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371

```
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggctct tccaagttcc tgtctgtgtg gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgag gtagagagga aactggggtt ggactgaaaa aggaacctgg tcacctatgg 540
aagtggtaaa atggcaaaga atttaacaac tgggtcaacg ttacaggggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780
```

236/292

```

ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgcatgag ctagaagcat 900
cacaggttga ccaataacca tgccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctatagactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta tttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatatat ctttgccttt ataacttttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg ttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa                                     1702

```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21) gene.

<400> 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat attttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccongataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgccnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng                    585

```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21) gene.

<400> 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

```

237/292

```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcatcagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g 451

```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c ttgggtgtc ctccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aagggaacaaa tggaccatt 300
caaatttcct cccagggacc aggccttatt aaccctggga aatgtcctta gctggtggg 360
gaaaggttgg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
accg 425

```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```

ggcgttccag ttcccacttg gaggccnttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttcctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttggg tgtactagt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacaccaaaa 300
ggggaaagct atttactgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaattttt aaagttactt ttgtcagagg caccaaagg 420
tttaaaactga ttcataaata aatatcngga cttoctcgat cttccaaaa aaaaaaaa 478

```


238/292

<210> 376
<211> 1794
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1794)
<223> cd44 antigen (homing function and indian
blood group system) (CD44) gene.

<400> 376
ccgcgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcacg ca gcctggggg 60
actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
aggtgtattc cacgtggaga aaaatggctg ctacagcatc tctcggacgg aggccgctga 180
cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
catcgatttt gagacctgca ggtatgggtt c atagaaggg catgtggtga ttccccggat 300
ccacccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360
ctcccagtat gacacatatt gcttcaatgc ttacagctcca cctgaagaag attgtacatc 420
agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480
tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
caaccctact gatgatgacg tgagcagcgg ctctccagtg gaaaggagca gcacttcagg 600
aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
catcttgcca tccctcttgg ccttggtctt gattcttgca gtttgcattg cagtcaacag 900
tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcattt 1020
ggtgaacaag gactcgctcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
cctgcagaat gtggacatga agattgggtt gtaacaccta caccattatc ttggaaagaa 1140
acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
cccaattaat aatcagcaag aatttgatcg ttcagttcca ctg gaggcc ttcacccctg 1380
ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440
tcccaccaca gctaaggaca tttccaggg ttaatagggc ctggtccctg ggaggaaatt 1500
tgaatgggtc catcttgccc ttccatagcc taatccctgg gcattgcttt ccactgaggt 1560
tgggggtgac tagttacac a ttttcaacag accccctcta gaaatttttc agatgcttct 1620
gggagacacc aaagggtgaa gctatttatc tgtagtaaac tatttatctg tgtttttgaa 1680
atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740
gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. cyclin-dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 377

```
ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtgggtt cattttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctcg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcagggt tgtaagcnc tccattattt 420
cacagcagct ggccatgctn ggagtccccc ca 452
```

<210> 378

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 3 (cdk2 -associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378

```
ggcacgagcg gcaactggtc tcgacgtggg ggggccanga ctgaagccca ngnttcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggt gtaaatttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472
```

<210> 379

<211> 639

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(639)

<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379

```
atggagccgc ccagttca at acaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccagggt tgtaaattha aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420
```

240/292

tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tcctactata cctgtctgac 480
 acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
 cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
 tcatacaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
 attggatcaa ctatttcttc agatcggttct gattcagagc gagaggagat tgaagtggat 120
 gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
 gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240
 gtgtcaaaact ttcatctact tcatagaacc cagcatgaca taacagtgc gggaaaatat 300
 tcaactgggcc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
 aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
 caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
 catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgcctgaggg ccctctccta cccagatacc gatgttatac tgatgtgttt 60
 ttcttttttt tttttttttt ttttaagtaat taagggtagt taaattattt aaagtatata 120
 aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180
 gaggcccgcg tcgccaccgc cgggtgccat ggagcgggtg aagatgatca acgtgcagcg 240
 tctgtctggag gctgccgagt ttttgagcgc ccgggagcga gagtgtgaac atggctacgc 300
 ctcttcattc ccgtccatgc cgagccccc actgcagcat tcaaagcccc cacggagggtt 360
 gagccgggca cagaacacac gcagcgggac gagcaacacc a gcaactgcc aacagatctac 420
 acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
 agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
 agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
 gaatttgga cgagaacaga gatttttaaa gtggcgactg gaacagctgc aggttcctca 660
 ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720
 ttcagagcga gagagagatt aagtggatgt tgaaagcaca gagttctccc atggagaagt 780
 ggacaatata agtaccacca gcacagtgat cattgatgac cacagcagcc tgccgagtat 840
 tgggagtgac gaggggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

241/292

```

agcatgacat aacagtgcag ggcaaaatat tcactgggcc aattcaatac aaacaatctc 960
ttaaattggg ttcatgatgc agtctctctt ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgacaaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttggtgt aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctggtt gtcatacta cattgagtag acacatttaa 1260
ggatgggggt atg aaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggatttaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcatgctct gcaaaggag agactcccat ga agcctttt 1500
gaaaggatc atcatgcagc tcaactttct gtggattcc atgctaagca agctaaccctt 1560
atcctgcatt gttagcacta ggcacccagc tgccacctct ccactctgct gcccttaggc 1620
cacatgggag cagtccatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
gggggggcaa aaggaaaaag ctcatg tgc ctctttgtct gcgtgggtca gaagagtgtg 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aacaaaaatg acatcttttt aaagcttatc cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat ttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccactctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttcatt ttctacagc cagtctctct 2160
cttctcaca gtccactgt gcagggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaat tttctagcct gcactttgat gtcatgtgtt ccctttgtct 2280
ttcaaaactc aagggtcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac tttaaataat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa 2416

```

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggata cgctaaatac tgctcagtag tttaaacgct cagataactca 300
gggacggaag gccctccctt gcccggggnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
<222> (1)..(439)
<223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383
aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
cgctatccaa atggcccgga ctaccagttg cataattatg gagatcatag ttccgtganc 120
gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180
atggatctca gcgtcggcng ctcngctcc ngcactttgg ctccggagag cgcgcccga 240
gctacgtnc aagccacgc gccnactcc aagcccaggt acagcnagcc ggccacgtcc 300
acgcactctn cctcancncg atccgctgcn ctgctccgnc gtnggccct tcgcccngga 360
ancgacanna ccaangggcg gaaaaactcc cttaaggca a ctccagcngg cgctcgggc 420
cgacngccgg aagcaccga 439

<210> 384
<211> 813
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(813)
<223> homeo box a5 (HOXA5) gene.

<400> 384
atgagctctt attttgtaaa ctcatcttgc ggtcgctatc caaatggccc ggactaccag 60
ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
cactccggca ggtacggcta cggctacaat ggcattggtc tcagcgtcgg ccgctcgggc 180
tccggccact ttggtccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcggcg 240
cccggccgagc ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
ctgccctgct ccgccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360
tccttaagca actccagcgg cgctcggcc gacgccggca gc acccacat cagcagcaga 420
gagggggttg gcacggcgtc cggagccgag gaggacgcc ctgccagcag cgagcaggcg 480
agtgcgcaga gcgagccgag cccggcgccg cccgcccac ccagatcta cccctggatg 540
cgcaagctgc acataagtca tgacaacata ggcggcccgg aaggcaaaaag ggcccggacg 600
gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
acctgcagaa ggaggattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720
atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
atggcccgcg caggaggggc cttccgtccc tga 81 3

<210> 385
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(447)
<223> 3' terminal sequence. x-box binding protein 1 (XBP1) gene.

<400> 385

243/292

```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gttaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaatac cttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttctacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447

```

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 386

```

aagaacctgt agaagatgac ctcgttccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttggggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtcocaa ggtattggag 420
acataattact ggaagtaaa gaaatattac tnataattgg ag 462

```

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

```

ggcgctgggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaacccggc cgacgggacc cctaaagttc tgcttctgtc ggggcagccc 120
gcctccgccg ccggagcccc ggcgggccag gccctgccgc tcatggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgagc tggaacagca agtggtagat 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 420
ggcctttagt ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctggttgct 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtc 540
gcagactca gactacgtgc acctctgcag cagggtgcagg ccagttgtc acccctocag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatacctgt 660
tgggcattct ggacaacttg gaccagtc tgttcttcaa atgcccttc ccagagcctg 720

```

244/292

```

ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcctcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaatc gaggaagcac ctctcagccc ctcagagaat gatcaccctg 960
aattcattgt ctcaagtgaag gaagaacctg tagaagatga cctcgttccg gagctgggta 1020
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tctaaggaat gatccaatac tgttgccctt ttcttgact attacactgc ctggaggata 1260
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gcagtcctaa gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
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tatgtaaagg tcattagaca aatgtcttga agtagacatg gaatttatga atgggtcttt 1560
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gtaagatcaa gaattctttg tgaaattata gaaatttact atgtaaat gc ttgatggaat 1740
tttttctgc tagttagct tctgaaagg gctttctcca tttattttaaa actacccatg 1800
caattaaaag gtacaatgca aaaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaatgtt gactcttgtg aaaagttaca tttatttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaagtgtc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttaa gagaattaga tgaaaacact 240
gaagtattat tngtatacct tggaaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggcctt aagtacagac ccccnaaatg gcagccttta tcncggggga 420
aatgcatatt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

```
ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatngnn cctctt 206
```

<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

```
tgccttgacc aggacttggg actttgcgaa aggatcgagg ggcccgagga ggtgttgagg 60
agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat gcggaaagct 120
gtgaagatac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
cattttaaaa ccatgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggga attgcctcat gatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtac tgaggaaagg gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaaatata catatttgc 660
ctttgcaaca tcttcagaag gccaatcatt gtcatttcag aaaaatgct aagaagttg 720
gaatcagggt ccaatttcgc ccctttgaaa gtgggtggaa tttacttgcc tctccactgg 780
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gcctctgca agaacaacct ggctgcccgc agcagaggagc tctgcatgga gtgtcagcat 2280
cccaaccaga ggatggggcc tggggccccc cgggggtgagc ctgccccga agaccccccc 2340
aagcagcgtt gccgggcccc cgctgtgat cattttggca atgccaagtg caacggctac 2400
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```

tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaaacagg tgggtcacct 2460
cctgcaagaa gtggggcctc gagctgtcag tcatcatggt gctatcctct gaaccctca 2520
gctgccactg caacagtggg cttaaggggtg tctgagcagg agaggaaaga taagctcttc 2580
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cctttcctga ggaccggca gaaatgcaga accatccatg gactgtgatt ctgaggc tgc 3060
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taaaaaatta gaataattta ctgggaagac gtgtaactct ttgggttatt actgtcttta 3180
cttctaaaga agttagcttg aactgaggag taaaagtgtg tacatatata atataccctt 3240
acattatgta tgagggattt ttttaaat t attgaaatg ctgccctaga agtacaatag 3300
gaaggctaaa taataataac ctgtttctg gttgtgttg gggcatgagc ttgtgtatac 3360
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ttaatgtgaa aaaaagtaat tatttatact tattataaaa agtatttgaa atttgcacat 4320
ttaattgtcc ctaatagaaa gccacctatt ctt tgttga tttcttcaag tttttctaaa 4380
taaattgtaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

```

<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

```

tttttttggtg cacaataatg atacatttat tgaaagagta tttttttttt aatacaaaaag 60
aaagctctgt acataggact gtgacctgt ccactattcc tgggtcagca tcccagggga 120
agtagaaacc actgacatac aactcacat tcaagcacac aactcactc aggcgcacac 180
accacacac acatacccca gagccaccga ggaagggaaa caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgcatgtcc tcccaaggcc acgctcacac 300
aacacacatt ataagcatt tgcctgattc actcactngg gtctgtcttt tgtgggaagg 360
agaggaagaa ttcatcaaag gtctcctccc catgggtngg gggagtggg agtgagtgag 420
tgatggtgga gtgaaacaag

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<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60
tgcagcaaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaat aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taatttgtag aggggccatg ccacncccc tctccccct ttngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatttt 360
cttaaccct aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
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ccgcggccag cagccctgc ccccggggg acgtgacgg ccgcccggcg cgccgcccta 120
gcagacggac agggggcgct gcgcgcggcc tggggcaacc cgggccac ag gggcaggaaa 180
gtgaggggcc aggtcggccc gggcgtgcag gggccccggg ttgcgagcgg cgcccgcggc 240
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gttaccgacc caagctgggg ccgcgg cggc tctgggcccgg ggctcggccc tggggggcag 420
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gccagactct ccaccccggt cag accccac aacagaccag agaagtagtg ccactggctt 1080
tgaagagaca gatctcacct accaggtgtc ggagtctgac agcagtgggg agaccaagga 1140

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cacactgaag cggcggttca cagtcaccaa cctgcggggt acaacctcca ccatccaaac 1200
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ccaccatcac tcaactcact cccactcccc caccatggg gaggagacct ttgatgaatt 3840
cttctctctc tcccc aaaa agacagaccc agtgagtga tcaggcaaa tgcttataat 3900
gtgtgtgtg tgagcgtggc cttgggagga catgcgtgtg tcagggatga gttgaggtga 3960
tatttttatg tgcagcgacc cttggtgttt cccttctcg gtggctctgg ggtatgtgtg 4020
tgtgggtgtg tgcgctgag tgagtgtgtg tgcttgaatg tgagtgtgta tgtc agtggg 4080
ttctacttcc cctgggatgc tgaccagga atagtggaca tggtcacagt cctatgtaca 4140
gagctttctt ttgtattaaa aaaaaatact ctttcaataa atgtatcatt tttgtgcaca 4200
g 4201

```

<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(563)
<223> 3' terminal sequence. sry (sex determining
region y)-box 9 (campomelic dysplasia, autosomal
sex-reversal) (SOX9) gene.

<400> 394
tttttaaatgc aatgtatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaagaa ggtaagtttc acggagagaa caaaagggtt ggggctggga gggaaacaag 120
tgaaacaaac aaaacacgaa cacaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccagggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgcttta agattttatt ctactgactt ctaaaactgt 300
taatataatct ttttttaaata aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atccctcca 420
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttggtg nccaacaca cacanacca nacacacnca caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa 563

<210> 395
<211> 3936
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3936)
<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395
ggagagccga aagcggagct cgaaactgac tggaacttc agtggcgcg agactcgcca 60
gtttcaaccc cgaaacttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120
cttttgctct ttttctccc ctctctctcc tctccaattc gctcccccc acttgagcg 180
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcgta gccggc cgac 240
gcgccagctt ccccgggagc cgcttgcctc gcatccgggc agccgagggg agaggagccc 300
gcgcctcgag tcccagagcc gccgcggtt ctgccttcc ccggccacca gcccctgcc 360
ccgggcccgc gtatgaatct cctggacccc ttcataaga tgaccgacga gcaggagaag 420
ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgccc 480
tcgggctccg gtcggacac cgagaacacg cgccccagc agaacacgtt cccaagggc 540
gagcccgatc tgaagaagga gagcgaggag gacaagtcc ccgtgtgcat ccgcgagggc 600
gtcagccagg tgctcaaagg ctacgactgg acgctggtgc ccatgccggt gcgcgtcaac 660
ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggcg 720
caggcggcgc gcaggaagct cgcggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc cttcgtggag 840
gaggcgagc ggctgcgctg gcagcacaag aaggaccacc cggattaca gtac cagccg 900
cgcgaggaga gtcggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaagccat ctcaaggcg ctgcaggccg actccacca ctctctctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080
ccaccacca ccccaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140
cgcccttgc agagggggg gcagagccc cctatcgact tccgcgacgt ggacatcggc 1200
gagctgagca gcacgtcat ctcaacatc gagacctcg atgtcaacga gtttgaccag 1260
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggt cacctacacg 1320
ggcagctacg gcatcagcag caccggggc acccggcgca gcgcgggcca cgtgtggatg 1380
tccaagcagc aggcgcgcgc gccaccccc cagcagcccc cacaggcccc gccggcccc 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
ccacaggcgc acacgctgac cacgctgagc agcagccgg gccg gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgccccaa 1620
cagatcgctt acagccccct caacctccca cactacagcc cctcctaccc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcggca 1740
ggccagggca cgggctct a ctccaccttc acctacatga acccgcgtca gcgccccatg 1800
tacaccccca tcgccgacac ctctggggtc ccttccatcc cgcagacca cagccccag 1860
cactgggaac aaccgctcta cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgacgatgg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca tttgtgtttt tttgtttttt tttttgttt tggtttttct tcttcttctt 2040
cttccttaaa gacatttaag ctaaaggcaa ctogtaccga aatttccaag acacaaacat 2100
gacctatcca agcgcatcac ccacttgttg ccaatcagtg gccaggccaa ccttggctaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgtgg 2220
aggatgatgg agaactgtgt gatcagtggt taaactctct ctgcctgttt ggactttgta 2280
attatttttt tagcagtaat taaagaaaaa agtcctctgt gaggaatatt ctctatttta 2340
aatattttta gtatgtactg tgtatgattc attaccattt tgaggggatt tatacatatt 2400
tttagataaa attaaatgct cttatttttc caacagctaa actactctta gttgaacagt 2460
gtgccttagc ttttcttgca accagagtat tttgttacag atttgcttcc tcttacaaaa 2520
agaaaaaaa aatcctgttg tattaacatt taaaaacaga atttgtttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
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gtaagcttta tgatatatat attttttaaa gaagagaaaa acaccttgag ccttaaaacg 2760
gtgctgctgg gaaacatttg cactctttta gtgcatttcc tctgccttt gcttggtcac 2820
tgcagtctta agaaagaggt aaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcc cgagcacact gcccccggtt gcctgcctgg gcccatgtg 2940
gaaggcagat gcctgctgcg tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacattc cacttgctaa aattatttat tttgtaagga gaggttttaa ttaaaacaaa 3060
aaaaaattct tttttttttt tttttttcca attttacctt ctttaaaata ggttggtgga 3120
gcttctctca aagggtatgg tcatctgttg ttaaattatg ttcttaactg taaccagtgt 3180
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ctacatcttc tcttgagtg agggaggcta cctggagggg atcagcccac tgacagacct 3540
taatcttaat tactgtgtg gctagagagt ttgaggattg ctttttaaaa aagacagcaa 3600
actttttttt ttatttaaaa aaagatatat taacagtttt agaagtcagt agaataaaat 3660
cttaaaagca tcataatatg gcacccctca atttctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tttttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgtt tcacttgttt cctcccagc cccaaacctt 3840
ttgtctcttc cgtgaaactt acctttccct tttctttctt cttttttttt ttgtatatta 3900
ttgtttacaa taaatataca tt gcattaaa aagaaa 3936

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<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tggaggaggg caaaggtggg actaggaggg 120

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tgaccgcgat gggccagatn ggagagaaac ttttcccacc cgggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgccgcccac ttgcagagaga tgccccgcag ncagcctgca cccccagcca ccccgagtgc 120
tgcccaccag ccccttgagc atcgccgact tcatcaatga tggcttgga g gctgcagata 180
gtgacccagc tgtgcgcgt tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cgggtggcggg gacntgagct ccatcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggctt ttctcctggg 420
gcactgctac ccagacacag aggccggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgccgtg tcaactcagcc tggacgcgt tcttcgggtc gggggtgcac tccggcccgg 60
ctcccgcctc ggccccgatg gacgccggt tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccacctg taccctggc 180
gccgggcgccc tgccctgagc cgcgtgcgga gggcctgggt catccccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtcggac aagcagcagc 300
tgggcagcgt catctacagc atccaggagc ccggcgtgga tgaggagccc cggggcgtct 360
tctctatcga caagttcaca gggaaggtct tctcaatgc catgctggac cgcgagaaga 420
ctgatcgctt caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttcctgcagg 540
aggcgttcac tggccgcgtg ctggagggtg cagtcccagg cac ctatgtg accagggcag 600
aggccacaga tggcagcagc cccgagacgg acaacgcagc gctgcggttc tccatcctgc 660
agcagggcag ccccgagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

252/292

```

ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgtc gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggc actctggttg 1260
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acgtgctcag cccggcgtcc cccttctca agggcggctg gtacagagcc atcgtcctgg 1440
cccaggatga cgctcccag ccccgcaccg ccaccggcac cctgtccatc gagatcctgg 1500
aggtgaacga ccatgcacct gtgtggccc cgccgcggcc gggcagcctg tgcagcgagc 1560
cacaccaagg ccaggcctc ctctgggcg ccacggatga ggacctgccc cccacgggg 1620
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tgaacgtgac cgtgtgccgc tgcggcaagg acggcgtctg cctgccgggg gccgcagcgc 1860
tgctggcggg gggcacaggc ctacgc ctgg gcgcactggt catcgtgctg gccagcgccc 1920
tcctgtctgt ggtgtgtgtc ctgtcgtgg cactccgggc gcggttctgg aagcagtctc 1980
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cgacagcgtc gagcctgcct ctgggaccgc cgccacttcg cagagatgcc ccgcagggcc 2160
gctgcacccc ccagccaccc cgagtgtgc ccaccagccc cctggacatc gccgacttca 2220
tcaatgatgg ctggagggt gcagatagtg acccagtggt gcgccttac gacacagccc 2280
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ccttctgtcc ggggtgggaa gaggtttctt ccatcgcccc catgcgggtc acc tccctag 2760
tccacacctt gcctcctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

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<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 399

```

tatctcacac tgtactttat tttctttcac aatattaact agacagacaa ggaaagttta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taaccatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttcag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc ttcaataca aaaacactta ttgtacactt 300
atttttattt aaacaaaaaa taac ccagat aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaagaaaag cttccccaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggccca cggagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctgaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

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<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 400
ggtattttaa caataaatgt gcagttttta ctaacaggat atttaatgac aaccttctgg 60
ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataataca agtcctttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaattg ctctgacaca 60
tgcacacgct cctgggcacg cctgctgcgn gtncgcttcc catga cccc agggccctct 120
atgcctcccc cccagggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240
agaacataaa agcatcttca acattogtca ttgagccaaa cgaaacacag tgtttggtc 300
aagagccggc gacactngca tcc ctatcca cagtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcanccgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402

```
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgaggggtct ccgcatttat tttcaaggcc aaaggaagtg 180
accctcggga aaacacccct gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttccacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcactca 360
gagtatcggg acccaagatg cactattggg gagtctgcc ccaccctggc aacttggcac 420
atggttcctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggttatttt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568
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<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403

```
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaatt toctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttgta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagttgc aggggtggggg aggactcaca atagtgcac ttgggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
acctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc ctttgttgt gcgaggtgt tttccgagg gtcacttcct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaaggagc agtttaaata accgtttcct 840
ttcatttact gtggcttctt aatcttttca caaataaa 878
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<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404

```
gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgccccctcg 60
ccccctgccc ggctttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcatc ctcccgctgc agcagcgct ccccgcccg gataaactct ctttattaca 180
attaatcanc g 191
```

<210> 405

<211> 245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405

```
ttttcaactt aaatgctttt attgacaatg tcttggaaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacggt 180
ttcatggaaa actgttaatg tccngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245
```

<210> 406

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(489)

<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406

```
gcgncgcgct caccgaaggg ngnangtaga cagcgggtca gaggcgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaataat ttgcccaggg acaaagtcaa 240
cacaaagaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga 300
gtcccggcag ttcttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgtccg tccacctgct cagcgagcc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcc a gagtagcttc gtctgaactt 480
gaacaagac 489
```

<210> 407

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

```
tggtttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcgt ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccagggga cgagccagtg ccgggaagga actgccggga ctcaccganc tgcncettaac 240
tggttctc                                     247
```

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

```
gccccccccc cagcctcctt cccctcctcc cgcccgcgcg tgetcccccc cctcgccgcc 60
gtctgctcgc tcgcccggcg gctcgcgtc ggccccctcc ctacagctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gctcggcgcg gccaccggcg ccgcgcggga gcggcccggg 180
ggccctcagc caggcccatg gcggcgcgcg ggcgcgctct cgggcccgggc accacgcggg 240
cgcgggggcg ggggcgcggg gccggggggcg ggtccccccg ggcgctgggc cgtgggcccgc 300
ctggaggggc gcgagttcga gtatctgatg aagaagcgct cggtgaccat cggccgcaac 360
tcgtcgagcg gctcgttgga cgtgagcatg ggccactcga gcttcatctc ccggcgccac 420
ctcagagatct tcacgccccg gggcgcgcgcg gccatggcgg ggccgctccg gagctgcgcg 480
ccgcgcagcc caggcccagc gccggcgggcg acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt ggacggcggtg ttccagaggg gcggggcgcc gccgctgcag ctgccgcgcg 600
tgtgcacatt caggttcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
ccacgggaac catcagcgct gcaaactcct gcccctccag cccccgggga gcggggtctt 840
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agcctgaaaa tgaaaag gaa gcttcagggtg gagacagccc gaaggatgat tcaaagccgc 960
cttactccta cgcgcagctg atagttcagg cgattacgat ggctcccgac aaacagctca 1020
ccctgaacgg gatttataca cacatcacta aaaattatcc ctactacagg actgcggaca 1080
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cctcgacctc ccagccaccc gtctgcaga cggttcacgt cgtccaccag atcccagcgg 1620
tgtcgtgcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680
```

257/292

```
ctgtggtcac cccggcagcc gtgctggccc ctcctaaggc agaggcccag gagaatggag 1740
accacagggg agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgccag ccgatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacaggc acctctaggt caacaccagc taccaataaa aactgtaaca caaaacggca 1920
ctcacgtggc atcagtcccc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca cagcatccg catcggcctc cctgccaca aagcgccaca 2040
acggtgacca gccggagcag ccggagctga agcggatcaa gacagaagac gccgagggca 2100
tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaagag ggtgtccaga 2160
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cggcctcccg ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaaccagct ggccttaaca ctcttaag acagaagtca cacttgaaca 2340
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tgtgttgact ttgtccctgg caaaatttcc cactctgagt aaaacaagtc tcggaattc 3059
```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 409

```
ttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggc cccttgtttg ttctggctg ggtcagggaa 180
ggcctgccgn ggggtggtggc a 201
```

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120
tctgctgctc cggggtggan ctggggtgtg ggatgcacgg cctcgtgggg gccgggcccgt 180
cctccagccc cgtcgtcccc tggccagccc cc ttgtcgtc gtcgggtccc tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

<210> 411

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha
(ARHGDI A) gene.

<400> 411

cctgaaccgc gcggccgaac cctccgggtgt cccgaaccag gctaagcttg agcatggctg 60
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120
actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
aggacgacga gagcctgcga aagtacaagg agggccctgct gggccgcgtg gccgtttccg 240
cagaccccaa cgtccccaac gtcgtggtga ctggcctgac cctggtgtgc agtcggccc 300
cgggcccccct ggagctggac ctgacggggc acctggagag cttcaagaag cagtcgtttg 360
tgctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480
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aggaggcacc caagggtatg ctggccccgg gcagctacag catcaagtcc cgcttcacag 600
acgacgacaa gaccgaccac ctgtcctggg agtggaaatc caccatcaag aaggactgga 660
aggactgagc ccagccagag gcgggcaggg cagagtgatg gacggaagac ggacaggcgg 720
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ccctcgatgg acaggcctga cccaccccac ctggggccag ccaggagccc cgcctggggc 1560
atcagtatgt attgcctccg tccgtgccgt ccctgggcca ctggctggcg cctcttcccc 1620
cagcctctca gtgccaccac cccgggcagc cttccctgac ccagccagg a caaacaaggg 1680
accaagtga cacattgctg agagccgtct cctataggta ccccgcccca tccccgtgt 1740
tggtgtgtg tctgccagga tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

<210> 412

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

259/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```
gctgcacaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtttcca gtttcatggg tcccagggtt aggttcctcc cagcggagggt gggagggcag 120
ccctcacacc tggcaccctt gattgcatac tcctggagga agtcgttgag ctgggcacag 180
gctgcccgct ggcggttgcn tccggcacag gcgttcagag ggcatctcct cgatccagct 240
attcgagtc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcaccttat ctctgcagaa gccaggttg 120
ctcttggtct ctcttctgt ggttcatctg ggg gtcccc tatcgggtgg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg tcttgagaaa cccatctcgt 240
aataatgtcc cctgctcccc aaaggtggac ttcacctta gctcagaaa agacttcgca 300
ctcctcagtc tccaggtgcc cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
agaggccctg aggtccagct ggtggcccat tcgccatggc taaaggactc tctgtccaga 420
acgacaaaac tccagggtat caacctgctc ttctcctctc gccgggggca cctctttttg 480
cagacggacc agcccattta caacctggc cagcgggttc ggtaccgggt ctttgctctg 540
gatcagaaga tgcgcccgag cactgacacc atcacagtca tgggtggaga ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg ccctcgtcca tcttccagga tgactttgtg 660
atcccagaca tctcagagcc agggacctgg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgagggtg aagaaatatg tccttcccaa ctttgagggtg 780
aagatcaccc ctggaaagcc ctacatcctg a cggtgccag gccatcttga tgaaatgcag 840
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aagctggtga atggacagag ccacatttcc ctctcaaagg cagagttcca ggacgccctg 1020
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atcattgagt ctccagggtg ggagatggag gaggcagagc tcacatcctg gtattttgtg 1140
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aacacagacg ggagcgacca agtcagcatt ccaataatta tccctcagac catctcagag 1380
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gccccacctt caggaggccc cg ggtttctg tctattgagc ggccggatc tcgacctcct 1500
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cattactact acatgatcct atcccagggg cagatcgtgt tcatgaatcg agagcccaag 1620
aggacctga cctcgggtct ggtgtttgtg gaccatcacc tggcaccctc cttctacttt 1 680
gtggccttct actaccatgg agaccacca gtggccaact cctgcgagt ggatgtccag 1740
gctggggcct gcgagggcaa gctggagctc agcgtggacg gtgccaagca gtaccggaac 1800
```

260/292

```

ggggagtccg tgaagctcca cttagaaacc gactccctag ccctggtggc gctgggagcc 1860
ttggacacag ctctgtatgc tgcaggcagc aagtcc caca agcccctcaa catgggcaag 1920
gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggtgg ggacagtgcc 1980
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<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
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tatttgagaa acccccaa at ttgctctgat ggcctttctt ctccatttgt catctctggg 120
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ggggctggta gagctggtca ttgggcaac a gagtctgctt gtctgnaagc tctcgactgg 360
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<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
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gcagaagcca aaaatatcac atggttttaa gatgggaaga tgatcggctt cctaactgaa 120
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aaaggatcac agaacaagtc aaaaccactc caagtgtatt acagaatgtg tcaganctgc 240
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aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

```
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<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence, v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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gccgccccca aaggccgct 43 9
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<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence, v-rel avian
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418

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ccggttcctc ccgccgtcag cctgctgcc agaccctgac ttcttctctg ggcaccgtgt 180
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<210> 419

<211> 2314

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419

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264/292

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<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 420

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gagcatcccg ctggattctt tttcaaagt caaaagaggt ttacaagtgt gtttcattaa 120
acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcatc ggcaaaagg 180
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<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 421

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<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(6450)

<223> estrogen receptor 1 (ESR1) gene.

<400> 422

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266/292

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gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 423

```
ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcaggggaa atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg tttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgccctt gcccactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggtat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaaggg gtagtagcat cctgcccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccagggtatc acaactgggtt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgctgcc aaaacagctg tcactgctac caatgtgtca gcccatggaa gccaaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttgc ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300
tggaggttgg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgac tccagcaat cgcattcccg ctgaccctgt 420
gcccagttg ggcaggggca ggagggaggg tttctctccc aacgctgaag cggtcagact 480
ggaggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1
(PBX1) gene.

```

<400> 425
cttccctgtt tatcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggtgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat. 360
gtgttgtgtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcggctggac aacatgctgt tagcggaaag cg tggcgggg 480
cctgagaagg gcggagggtc ggcggcagcg gcggcagcgg cggcggcttc tggaggggca 540
ggttcagaca actcagtga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagc aggcctgca acgagttcac caccacgtg 660
atgaatcttc tgcgagagca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttcccga tttctggatg cgcggcggaa gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccaaagaat gtggcatcac agtctcccag 960
gtatcaaact ggtttgaaa taagcgaatc cgttacaaga agaäcatagg taaatttcaa 1020
gaggaagcca atatttatgc tgccaaaaca gctgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaaag ctaactcgcc ctcaactccc aactcggctg gttcttcca g tcttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca cagggtggata cccttcgcca tgttatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtcc gcagggcatc 1320
agtgtaatg gaggttgga gga tgctact accccttcat cagtgaacct ccctacagaa 1380
ggccctgga gtgttctact tgatacctcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc cccagttggg gcaggggcag gagggagggt ttctctccca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctcttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct tttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg ttttctcat cttccctgcc 1680
cctgtgcctc tgcctagac ttcccggggt ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli-kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)

(GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tactttaggg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaatct cttcaactcc taatgatttc cggttggttc agtctttttt 240
tcttaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgtg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aaactatgga aaagggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

```

269/292

<210> 427
 <211> 239
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(239)
 <223> 5' terminal sequence. gli -kruppel family
 member gli3 (greig cephalopolysyndactyly syndr ome)
 (GLI3) gene.

<400> 427
 ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
 tgtctctatt taaaaaaciaa aaagcctggg gtgggtgggtgc atgcctgtag tctcagcctc 120
 ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
 agagacaggg tttcaccacg ttgccacagg cagtcttgaa ctctgacct caagtgatc 239

<210> 428
 <211> 5054
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5054)
 <223> gli-kruppel family member gli3 (greig
 cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
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 gcccagtccc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
 tgctccactc gaacagatgt gagcgagaaa gccgttgcc tccagcaccac ttctaagag 180
 gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
 cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
 gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
 ccgtaccgag ggacgggtt tt tgccatggac cccaggaatg gttacatgga gcccactac 420
 caccctctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
 gagggccggt accattacga tccatctccg attcctc

cat tgcataatgac ttccgcctta 540
 tctagtagcc ctacgtatcc ggacctgccc ttcattagga tctcccaca ccggaacc cc 600
 gctgctgctt ccgagtctcc ctccagccct ccacatccct acattaatcc ctacatggac 660
 tatatccgct ccttgacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
 agccctacag atgcgcccc tgcaggagtc agccagcag aatactatca tcagatggcc 780
 ctgctaactg gccagcgag cccctatgca gacatt attc cctcagctgc caccgcggc 840
 acgggggcca tccacatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900
 aggctgtcag ccaggccgag ccgaaaacgt aactgtcca taccacct ctccgatcat 960
 agctttgacc ttcagacat gataaggagc tctcccaact ccttggtcac gattctcaat 1020
 aattcccgtg gca gctcttc agcaagtggc tccatgggtc acttatctgc aagtgaatc 1080
 agccctgctt tgagcttcac ctactcttcc ggcggcgtct ctctccacat gcacagcag 1140
 atccctaagc gacaacagag cttagggtca gcctttggac acagccctcc actcatccac 1200
 cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggccc ttctgagtc tccagaaca agccacagag tgagtctgca 1320
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 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440
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 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560
 aacgaccata ttcattggaga gaagaaggag ttctgtgtgca ggtggctgga ctgctcaaga 1620
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 tccctccgga aacatgtgaa gacagtgcac ggcccagagg ctcatgtcac caagaagcag 1980
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 agcaccctca tgcaagggag cgggggccag ctgaatttcg gcctgccggt agcgcctaat 3960
 gagtacgctg gcagcatggt gaatggcatg cagaaccagg acccagtggg acaggggtac 4020
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 cagatgcttg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140
 tgcctgccag gggctcacgg catgggcagc cagccgtcaa gcttggcagt tgtcaggggc 4200
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 ggtgctaate aggtgacaag cacagtggac agcctcgaca gccatgacct ggaaggggta 4560
 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620
 ctgagcccaa gtatcattca gaacctttcc catagctcct cccgcctcac cagcctcgg 4680
 gcgtccctcc cattcccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc acctaaactga 4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
aggagagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaat ttggccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaaac agttaagtgc agctcgggtga gtcccggcag 120
ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgct cagcgagcc acatgctgaa atggaggtgg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTRACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NCACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431

AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432

<211> 242

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. Similar to NM_022641 Homo sapiens chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432

ATTCGGCACG ATGACTGGCC AGGGTATAAA AAGGGCCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTCCGT TATCCAGGGT TTTGACCAC GCTATGCTNC 240
AA 242

<210> 433

<211> 329

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(329)

<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433

AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACGAC GCCTGCCAGG GNATTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG 247

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT 63

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG 190

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATATAA TGCATTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCCACG GNGACATGTG GCCTTCTAGC TTNAATNCTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTC AATAACAGGT GAGNNAAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTTCTTGA GCTGCAGCTG GCGGGTAGGG CNCGGGGCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGGNGT 337

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTCCGTCT G GG 223

<210> 443

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<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggttc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctectac accggcngcc cctgcaccag cccctcctcg gccctgtca tcttctgtcc 180
cttcccagan aacctaccag ggcagctacg gtttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggtta cagtgaggac 60
cccacagtac ccctgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cgccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgacct gctggtgcca ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtaaaa gagtttttgc cttt gggggt gccgtgggag aaccccgagt 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcatct tgcgccccct gctggtngaa 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240
ntcgaagggg ganttgggna ngtagggtn gtn gcttgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tgttcacaac tataaattta 60
aaccttttgc actaaaaaaa cacaaaaaca caaacacaa accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180
tccttggcaa ctgtaatgtt ttngcaccgg ntgatctccc gcnggggggta ctagtaatga 240
ctggctgccc gtgtaggag atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448
<211> 393
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(393)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(393)
<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448
aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggtaaggga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa ttctacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgcctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449
<211> 217
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(217)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(217)
<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449
ttacntgggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60
tctggnctca cctttgtctc agctaaatgt agccgcaccc gggacacagt ttgtgccaca 120
tgtgccgaga attcctacaa cgagc actgg aactacctga ccatctgcca nctgtgccgc 180
ccctgtgacc cagtgtatggg cctcgnctga gantgcc 217

<210> 450
<211> 157
<212> ADN

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

nattcggcaa cgnggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca 157

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis-related cysteine protease
(CASP4) (ex CASP1)

<400> 451

gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtcct ctgacagcac attcttggtg ctcattgtctc atggcctcct ggagggaatc 120
tgcggaactg tgcattgatga gaaaaaacca gatgtgctgc ttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggttgca gaggggtgcaa accttggggg aantttgggg tc 282

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactota cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcc 120
ctgtgctgtg tgtgacgtga ccggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggtccttc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttncgtg gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaagggtg gatggggccc agcnacagct ttgnaccc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgtccc cggctgtccc tcacctgtg gcaagtacat ctctgtcgcc gagtgcctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgcg tgccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc 180
ctacacgtg gagcagcagg acgggatgga ccgtacctc atctatgtg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtcc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

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<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha
isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgn c aagcagnacg 60
nctnacaaca tcaaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggaagt aaaagatctt ctgncctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggaact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic
subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagcaggaac 60
cggcggcggc gngtgcgngt aggcccggtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcgggnggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccagnnac 30 0
ngnccgngga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456
cagcctcccg cgctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatggttata 120
actacactct ctccaagaca gagttcctaa gtttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatggta gctagatttc tcagaatttc ttaatctgat tggtaggcta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360
gggcoctggg cctttcaaac ccacccccctn ttcctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtg ccaactggtc 480
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaccgcta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatggggcc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tncctaag aacctnaat 359

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

<220>

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<221> misc_feature

<222> (1)..(1251)

<223> endothelin 1 (EDN1)

<400> 458

```
ggagctgttt acccccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcgcg tgcgcctgca gacgtccgc tcgctgcctt ctctcctggc 180
aggcgtgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgc agcgcttga gggacctgaa gctgttttcc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaacag cagtcttagg cgctgagctc 420
agcgcggttg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cgggtccaagc gctgctcctg ctgcctcctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccag caggttggtc cgtatggact tggaaagccct 600
aggccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggtcg aagacattat ggagaaagac tgggaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtgga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaa acaaaccagg tcggagacca tgagaacacg cgtcaaatca 900
tcttttcatg atcccaagct gaaaggcaag cctccagag agcgttatgt gaccacaac 960
cgagacattt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cggagagccc 1020
tgtggccgac tctgactct ccacctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttactg gcttccatca gtggtaactg ctttggctc tcttttcac 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattogaatt c 1251
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<210> 459

<211> 2145

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2145)

<223> 3' terminal séquence

<220>

<221> misc_feature

<222> (1)..(2145)

<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

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cggcagaact gggaccaccg ggggtggtga ggcggcccgg cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctcctcatt ccctgcgccc 120
ccttctctc cggaagcccc caggatggtg aggtggttcc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggtg gcttctctggc tcggccagct 240
cgcaagaacc aggtgactt ctgcctctcc gtccaggtgg gggatcaggt gacctatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag cagggtgtgg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtaccc gctgaactgc tccgatccca ctagttagag gtggtaccat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttctg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgag accttcgaca gcctcacgga cctgggtggag 720
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```

catttcaaga agacggggat tgaggaggcc tcaggcgccct ttgtctacct gcggcagccg 780
tactatgcc a cgaggggtgaa tgcggtgac attgagaacc gagtgttgga actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagtttga gagtttgca 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccttt gaccacagcc gactgatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggcagatggc gtggcaggag aacagccgtg tcatcgatcat gaccacccga 1200
gaggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatggggtc cccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcacg caggggccat catcgtgcac 1500
tgccagccg gcacggcg cgacaggcacc atcattgtca tcgacatgct catggagaac 1560
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aagaggaaat gagcggctgt gtcctcaggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gcccattct tt tgtaattt 2040
aaatggctgc atccccccca cctctccctg acctgtata tagccagcc agggcccag 2100
cagggccaac ccttctctc ttgtaaataa agccctggga tcaact 2145

```

<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

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caccagggca gccgagagac ctccctcccg cccctcccat gccgcctcc ctccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cactccgtc cgccgctgcc 180
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gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcggcagca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtgcgct cgctggaggc ccacatgtac ccggaaaagc tcaaggtgat tgcgcagcag 840

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```
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ggagaagcta ttatatttt ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
ccttgttaaa gaaacaaaat aaa gtttgta ctttgtttt taaaaaaaa 2149
```

<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

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ctgccctcac ctctcccccg aaaacccctt attagccaa aggaagg agg tcaggggaac 180
gctctcccct ccccttcaa aaaaacaaa cagaaaaacc cttttccagg ccggggaaag 240
caggagggag aggggccgcc gggtggcca tggagctgct gtgccacgag gtggaccgg 300
tccgcagggc cgtgcgggac cgcaacctgc tccgagacga ccgcgtcctg cagaacctgc 360
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aactcaaaaga gaccagccg ctgaccgcg agaagctgtg catttacacc gacaactcca 660
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tggcagctgt cactcctcat gacttcattg agcacatctt gcgcaagctg cccagcagc 780
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<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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gctcccaccc cggcccagcc ccgaccggc ccggtcaggc ccatactca gtagccacga 120
tggagggtgat gaacctgat gagcagccta tcaagggtgac tgagtggcag cagacataca 180
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tgctggccac ccagggtgag gggcaggcca ccaacctgca gcgactggcc gagccgtccc 480
agctgctcaa gtgcggccatt gtgcatctca tcaactacca ggacgatgcc gagctggcca 540
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aggcggccat. gattgtgaac cagctgtcga agaaggaggc gtcgcgccgg gccctgatgg 660
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<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA-damage-inducible, alpha
(GADD45A)

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cgaggcgagg tccggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120
cggtctggcac aggagagga gcccgggcgg gcgaggggcg gccggagagc gccagggcct 180
gagctgccgg agcggcgccct gtgagtgagt gcagaaagca ggcgcccgcg cgctagccgt 240
ggcaggagca gcccgcacgc cgcgtctctt ccctgggcga cctgcagttt gcaatatgac 300
tttgaggaa ttctcggctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360
cctggaggaa gtgctcagca aagccctgag tc agcgacg atcactgtcg ggtgtacga 420
agcgccaag ctgctcaacg tcgaccccg taacgtggtg ttgtgcctgc tggcggcgga 480
cgaggacgac gacagagatg tggctctgca gatccacttc accctgatcc aggcgttttg 540
ctgcgagaac gacatcaaca tcctgcgcgt cagcaaccgg ggcgggctgg cggagctcct 600
gctcttgagg accgacgtg gcccgcgggc gagcgagggc gccgagcagc ccccgacact 660
gcactgcgtg ctggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720
acttatttgt ttttgccggg aaagtgcgta catggatcaa tgggttccag tgattaatct 780
ccctgaacgg tgatggcatc tgaatgaaaa taa ctgaacc aaattgcact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900
tgatgccaag gggctgagtg agttcaacta catgttctgg gggcccggag atagatgact 960
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc cggggcgcgt ttccgggtgct ggcggctgca gccggagttc 60
aaacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcgatcaaa 120
ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggctggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggtctggga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360
gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
ggcaggaaca ttatacatgg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
tgacaggagg gcagaccaca ttgcttttca catccatttc ccctccttcc catgggcaga 600
ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gaggggaagc 660
tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
cttcctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
agccggaatg gcatgttctt gaagcccccac ttccacaagg actggcagcg gcgcgtggcc 120
acgtggttca accagccggc ccgtaagatc cgcagacgta aggcccgga agccaaggcg 180
cgccgcatcg ccccgcgccc cgctcggtt cccatccggc ccatcgtgcg ctgccccacg 240
gttcggtacc acacgaaggt gcgcgcgggc cgcggttca gcctggagga gtcagggtg 300
gccggcattc acaagaaggt ggcccggaac atcggcattt ctgtggatcc gaggaggcgg 360
aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
ctcatcctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480
ctgaaactgg ccaccagct gaccggacgg gtcatgcccg tccggaacgt ctataagaag 540
gagaaagctc gagtcatcac tgaggaagag aagaatttca aagccttcgc tagtctccgt 600
atggcccgtg ccaacgcccg gctcttcggc atacgggcaa aaagagcaa ggaagccgca 660
gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttggaatc agtcgggcag 720
tcatgctggg tctccacgtg gtgtgtttcg tggaacaac tgggcctggg atggggcttc 780
actgctgtga cttcctcctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
tgataaatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
aaaacggttt tcttgtgggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctctgcagc tggccccgc 60
ccaggccctt gtctccagc ctgatgcccc tggccaccag aggaaagtgg tgtcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggctgctgc cctgacgatg gcctggagtg tgtgccact gggcagcacc aagtccgat 300
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaa ggacagtgtg gtgaagccag acagggtgtg 420
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480
accctcccca gctgacatca cccatccac tccagcccca ggccctctg cccacgtgc 540
accagcacc accagcgccc tgacccccg acctgccgc gccgtgccg acgccgcagc 600
ttctccgtt gccaaaggcg gggcttagag ctcaaccag acacctgcag gtgccggaag 660
ctgcgaagg gacacatggc ttttcagact cagcaggggt acttgctca gaggctatat 720
cccagtggg gaacaaagag gaggctggt aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgtgttct ggattcccgt 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggcacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgtggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300
tgtgtcagt gttatatcct ccaggaatac tggccagagg gctgtgtg a agtttgctgc 360
tgccactgga gccactcaa ttgctggccg cttcactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc cagggcttct tgtggttact gacccaggg ctgaccacca 480
gcctctcacg gaggcatctt atgttaacct acctaccatt gcgtgtgtg acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaagtgtg tggatgtgtg ctccgggaagt tctgcgcatg cgtggcacca ttcccggtga 660
acacccatgg gaggatcatg ctgatctgta cttctacaga gatcctgaag agattgaaaa 720
agaagagcag gctgtgtgtg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgct cctgagttca ctgctactca gcctgaggtt gcagactggt ctgaagggtg 840
acagggtgcc tctgtgccta ttacgaatt ccctactgaa gactggagcg ctgagcctgc 900
cacggaagac tgggtctgcag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960
tgactgtgtt taagctg ttc ttgcataggg tottaagcag catggaaaaa tgggtgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcacg atgactggcc aggggtataaa aagggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccactcaggg tctgtggca gtcacctag tggcaatggc 120
tccaggctcc cggaaagtc ctgatectgg nttttgncct nctctnactg ccctggnttn 180
aanaagctng tgcntccaa ancgttcgt tatccagggt ttttgaccac gctatgctnc 240

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